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OM protein - protein search, using sw model

Run on: August 24, 2006, 23:51:43 ; Search time 51 Seconds
(without alignments)

34.326 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 20

Sequence: 1 YGRKVRQRKKPASADGHR 20

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size : 1

Total number of hits satisfying chosen parameters: 641544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :	Issued Patents_AA.*	Description
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	12	60.0	12	2	US-09-556-121-14	Sequence 14, App1
2	12	60.0	12	2	US-09-653-182-21	Sequence 15, App1
3	11	55.0	11	1	US-08-706-741B-54	Sequence 15, App1
4	11	55.0	11	1	US-08-924-695A-54	Sequence 15, App1
5	11	55.0	11	2	US-09-208-66-2	Sequence 2, App1
6	11	55.0	11	2	US-09-296-089-37	Sequence 37, App1
7	11	55.0	11	2	US-09-837-063-2	Sequence 2, App1
8	11	55.0	11	2	US-09-742-42-1	Sequence 1, App1
9	11	55.0	11	2	US-09-434-345-2	Sequence 2, App1
10	11	55.0	11	2	US-09-632-387A-22	Sequence 22, App1
11	11	55.0	11	2	US-09-632-77A-4	Sequence 4, App1
12	11	55.0	11	2	US-09-612-033B-15	Sequence 15, App1
13	11	55.0	11	2	US-09-780-070-37	Sequence 37, App1
14	11	55.0	11	2	US-09-775-052A-2	Sequence 2, App1
15	11	55.0	11	2	US-09-911-842A-6	Sequence 6, App1
16	11	55.0	11	2	US-09-97-465B-2	Sequence 2, App1
17	11	55.0	11	2	US-10-083-889-17	Sequence 17, App1
18	11	55.0	11	2	US-09-551-976-37	Sequence 37, App1
19	11	55.0	11	2	US-09-265-107-75	Sequence 75, App1
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21	11	55.0	11	2	US-09-545-433-14	Sequence 14, App1
22	11	55.0	11	2	US-10-031-505-12	Sequence 12, App1
23	11	55.0	11	2	US-10-144-549-6	Sequence 6, App1
24	11	55.0	11	2	US-09-825-414-91	Sequence 91, App1
25	11	55.0	11	2	US-10-286-996-22	Sequence 22, App1
26	11	55.0	11	2	US-09-909-474D-5	Sequence 5, App1

ALIGMENTS

RESULT 1

US-09-656-121-14

; Sequence 14, Application US/09656121

; Patent No. 6706592

; GENERAL INFORMATION:

; APPLICANT: CONJUCHEM, INC.

; ERBIN, ALAN M.

; FLESER, ANGELICA

; ROBITAILLE, MARTIN

; MULNER, PETER G.

; BRIDON, DOMINIQUE P.

; TITLE OF INVENTION: PULMONARY DELIVERY FOR BIOCONJUGATION

; CURRENT APPLICATION NUMBER: US/09/656,121

; CURRENT FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/152,681

; PRIOR FILING DATE: 1999-09-07

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 14

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence : Synthetic

; OTHER INFORMATION: Peptide

US-09-656-121-14

Query Match 60.0%; Score 12; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.4e-05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKVRQRKKR 1.2

Dy 1 YGRKVRQRKKR 1.2

RESULT 2

US-09-656-121-15

; Sequence 15, Application US/09656121

; Patent No. 6706592

; GENERAL INFORMATION:

; APPLICANT: CONJUCHEM, INC.

; ERBIN, ALAN M.

; FLESER, ANGELICA

; ROBITAILLE, MARTIN

; MULNER, PETER G.

; BRIDON, DOMINIQUE P.

; TITLE OF INVENTION: PULMONARY DELIVERY FOR BIOCONJUGATION

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FILE REFERENCE: REDC-1810
CURRENT APPLICATION NUMBER: US/09/6556,121
CURRENT FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/152,681
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 15
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence:Synthetic
OTHER INFORMATION: Peptide
US-09-6556-121-15

Query Match      60.0%; Score 12; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 YGRKKRKQRKK 12
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Db    1 YGRKKRKQRKK 12
      ||||| | | |

RESULT 3
US-08-706-741B-54
Sequence 54, Application US/08706741B
Patent No. 5955593
GENERAL INFORMATION:
APPLICANT: KORMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
ZIP: 63146
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971798
TELECOMMUNICATION INFORMATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,741B
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 9655017
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6992
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-706-741B-54

Query Match      55.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 YGRKKRKQRKK 11
      ||||| | | |
Db    1 YGRKKRKQRKK 11
      ||||| | | |

RESULT 4
US-08-944-695A-54
Sequence 54, Application US/08924695A
Patent No. 5998583
GENERAL INFORMATION:
APPLICANT: KORMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,695A
FILING DATE: 09-SEP-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971798
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6992
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-924-695A-54

Query Match      55.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 YGRKKRKQRKK 11
      ||||| | | |
Db    1 YGRKKRKQRKK 11
      ||||| | | |

RESULT 5
US-09-208-966-2
Sequence 2, Application US/09208966
Patent No. 6221355
GENERAL INFORMATION:
APPLICANT: Dowdy, Steven F.
TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
FILE REFERENCE: 48881/1742
CURRENT APPLICATION NUMBER: US/09/208,966
CURRENT FILING DATE: 1998-12-10
EARLIER APPLICATION NUMBER: 60/082,402
EARLIER FILING DATE: 1998-04-20
EARLIER APPLICATION NUMBER: 60/059,012
EARLIER FILING DATE: 1997-12-10
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 2
TYPE: PRT
ORGANISM: human
US-09-208-966-2

Query Match      55.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 YGRKKRKQRKK 11
      ||||| | | |
Db    1 YGRKKRKQRKK 11
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Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Organism: Human immunodeficiency virus

Qy 1 YGRKERRQRRR 11
 Db 1 YGRKERRQRRR 11

RESULT 6
 US-09-296-089-37
 Sequence 37, Application US/09296089
 GENERAL INFORMATION:
 APPLICANT: Blaschuk, Orest W.
 APPLICANT: Byers, Stephen
 APPLICANT: Gour, Barbara J.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
 TITLE OF INVENTION: BETA-CATENIN MEDIATED GENE EXPRESSION
 FILE REFERENCE: 100086_411
 CURRENT APPLICATION NUMBER: US/09/296,089
 CURRENT FILING DATE: 1999-04-21
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: Fast-SEQ for Windows Version 3.0
 SEQ ID NO: 37
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus
 US-09-296-089-37

Query Match 55.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Organism: Human immunodeficiency virus

Qy 1 YGRKERRQRRR 11
 Db 1 YGRKERRQRRR 11

RESULT 7
 US-09-837-863-2
 Sequence 2, Application US/09837863
 GENERAL INFORMATION:
 APPLICANT: Greene, Amy
 APPLICANT: Zhou, Hua
 APPLICANT: Thode, Silke
 APPLICANT: Jarnigan, Kurt
 TITLE OF INVENTION: Vector and Method for Targeted Replacement and Disruption
 TITLE OF INVENTION: of an Integrated DNA Sequence
 FILE REFERENCE: 025..JUS
 CURRENT APPLICATION NUMBER: US/09/837,863
 CURRENT FILING DATE: 2001-04-17
 PRIOR APPLICATION NUMBER: US 60/198,498
 PRIOR FILING DATE: 2000-04-18
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 2
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus
 US-09-837-863-2

Query Match 55.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Organism: Human immunodeficiency virus

Qy 1 YGRKERRQRRR 11
 Db 1 YGRKERRQRRR 11

RESULT 8
 US-09-660-742-1
 Sequence 1, Application US/09660742
 GENERAL INFORMATION:
 APPLICANT: Collier, Alan V.
 APPLICANT: Beer, Steven V.
 TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND TECHNIQUES FOR DELIVERING TO
 TITLE OF INVENTION: EUKARYOTIC CELLS BACTERIAL PROTEINS THAT ARE SECRETED
 TITLE OF INVENTION: VIA TYPE III SECRETION SYSTEMS
 FILE REFERENCE: 1960314021
 CURRENT APPLICATION NUMBER: US/09/660,742
 CURRENT FILING DATE: 2000-09-13
 PRIOR APPLICATION NUMBER: 60/153,507
 PRIOR FILING DATE: 1999-09-13
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-660-742-1

Query Match 55.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Organism: Homo sapiens

Qy 1 YGRKERRQRRR 11
 Db 1 YGRKERRQRRR 11

RESULT 9
 US-09-434-345-2
 Sequence 2, Application US/09434345
 GENERAL INFORMATION:
 APPLICANT: Boulikas, Teni
 TITLE OF INVENTION: THERAPY FOR HUMAN CANCERS USING
 TITLE OF INVENTION: CISPLATIN AND OTHER DRUGS OR GENES ENCAPSULATED INTO
 TITLE OF INVENTION: LIPOSOMES
 FILE REFERENCE: TB 2001-00
 CURRENT APPLICATION NUMBER: US/09/434,345
 CURRENT FILING DATE: 1999-11-05
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 2
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Human Immunodeficiency Virus
 US-09-434-345-2

Query Match 55.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Organism: Human Immunodeficiency Virus

Qy 1 YGRKERRQRRR 11
 Db 1 YGRKERRQRRR 11

RESULT 10
 US-09-632-287A-22
 Sequence 22, Application US/09632287A
 GENERAL INFORMATION:
 APPLICANT: Hsu, Hailing
 APPLICANT: Woodin, Scott K
 APPLICANT: Boyle, William J
 TITLE OF INVENTION: Fhm, A No. 6521422el Member of the TNF Ligand Supergene Family
 FILE REFERENCE: 01017/3550A
 CURRENT APPLICATION NUMBER: US/09/632,287A
 CURRENT FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: US 60/147,294
 PRIOR FILING DATE: 1999-08-04

NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 22
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Peptide from the HIV TAT protein
 US-09-632-287A-22

Query Match 55.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRR 11
 Db 1 YGRKKRQRR 11

RESULT 11
 US-09-632-277A-4
 / Sequence 4, Application US/09632277A
 / Patent No. 6597116
 / GENERAL INFORMATION
 / APPLICANT: Hsu, Hailiang
 / TITLE OF INVENTION: NTR3 A No. 6599716el Member of the TNF-Receptor Supergene Family
 / FILE REFERENCE: 01017/35549A
 / CURRENT FILING DATE: 2000-08-03
 / PRIOR APPLICATION NUMBER: US 60/147,297
 / PRIOR FILING DATE: 1999-08-04
 / NUMBER OF SEQ ID NOS: 4
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 4
 / LENGTH: 11
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: HIV TAT Peptide
 US-09-632-277A-4

Query Match 55.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRR 11
 Db 1 YGRKKRQRR 11

RESULT 12
 US-09-612-031B-15
 / Sequence 15, Application US/09612031B
 / Patent No. 6627199
 / GENERAL INFORMATION
 / APPLICANT: Sariis, Chris
 / TITLE OF INVENTION: Isolation, Identification, and Characterization of
 / TITLE OF INVENTION: tmr2, a No. 6627199el Member of the TNF-Receptor Superfamily
 / FILE REFERENCE: 01017/35434A
 / CURRENT APPLICATION NUMBER: US/09/612,033B
 / CURRENT FILING DATE: 2000-07-07
 / PRIOR FILING DATE: 1999-07-09
 / NUMBER OF SEQ ID NOS: 15
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 15
 / LENGTH: 11
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: peptide
 US-09-612-033B-15

Query Match 55.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRR 11
 Db 1 YGRKKRQRR 11

RESULT 13
 US-09-780-070-37
 / Sequence 37, Application US/09780070
 / Patent No. 6632656
 / GENERAL INFORMATION
 / APPLICANT: Burke, James
 / APPLICANT: Strittmayer, Warren
 / APPLICANT: Nagai, Yoshitaka
 / TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT
 / TITLE OF INVENTION: AND METHODS OF USE THEREOF
 / FILE REFERENCE: 5405-242
 / CURRENT APPLICATION NUMBER: US/09/780,070
 / CURRENT FILING DATE: 2000-02-09
 / PRIOR APPLICATION NUMBER: 60/189,781
 / PRIOR FILING DATE: 2000-03-16
 / NUMBER OF SEQ ID NOS: 40
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO 37
 / LENGTH: 11
 / TYPE: PRT
 / ORGANISM: Human immunodeficiency virus
 US-09-780-070-37

Query Match 55.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRR 11
 Db 1 YGRKKRQRR 11

RESULT 14
 US-09-775-052A-2
 / Sequence 2, Application US/09775052A
 / Patent No. 6615501
 / GENERAL INFORMATION
 / APPLICANT: Dowdy, Steven F.
 / TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
 / FILE REFERENCE: 48881/1742
 / CURRENT APPLICATION NUMBER: US/09/775,052A
 / CURRENT FILING DATE: 2001-12-05
 / PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/208,966
 / PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10
 / PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,012
 / PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-10
 / NUMBER OF SEQ ID NOS: 57
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 2
 / LENGTH: 11
 / TYPE: PRT
 / ORGANISM: human
 US-09-775-052A-2

Query Match 55.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00013; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRR 11
 Db 1 YGRKKRQRR 11

RESULT 15
US-09-911-842A-6
Sequence 6, Application US/09911842A
Patent No. 6656707
GENERAL INFORMATION:
APPLICANT: Angen Inc.
FILE REFERENCE: 01017137592
TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/911,842A
CURRENT FILING DATE: 2001-07-24
PRIORITY NUMBER: US 60/222,438
PRIOR FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-911-842A-6

Query Match 55.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy YGRKGRQRQQRR 11
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Db YGRKGRQRQQRR 11

Search completed: August 24, 2006, 23:53:08
Job time : 52 secs

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2	12	60.0	12	4 US-10-756-774-14	Sequence 14, Appli
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4	12	60.0	20	5 US-10-930-192-4	Sequence 4, Appli
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6	12	60.0	20	5 US-10-930-192-12	Sequence 12, Appli
7	12	60.0	20	6 US-11-021-928A-276	Sequence 276, Appli
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21	11	55.0	11	3 US-09-935-866-24	Sequence 24, Appli
22	11	55.0	11	3 US-09-928-175-25	Sequence 25, Appli
23	11	55.0	11	3 US-09-995-542-13	Sequence 13, Appli
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25	11	55.0	11	3 US-09-984-183-4	Sequence 4, Appli
26	11	55.0	11	3 US-09-949-196-15	Sequence 15, Appli
27	11	55.0	11	3 US-09-948-018-22	Sequence 22, Appli

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	5 US-10-814-109-2	Sequence 2, Appli
2	12	60.0	12	4 US-10-756-774-14	Sequence 14, Appli
3	12	60.0	12	4 US-10-756-774-15	Sequence 15, Appli
4	12	60.0	20	5 US-10-930-192-4	Sequence 4, Appli
5	12	60.0	20	5 US-10-930-192-5	Sequence 5, Appli
6	12	60.0	20	5 US-10-930-192-12	Sequence 12, Appli
7	12	60.0	20	6 US-11-021-928A-276	Sequence 276, Appli
8	12	60.0	20	6 US-11-021-928A-363	Sequence 363, Appli
9	12	60.0	20	6 US-11-021-928A-364	Sequence 364, Appli
10	12	60.0	22	3 US-09-049-196-22	Sequence 22, Appli
11	12	60.0	22	3 US-09-049-196-34	Sequence 34, Appli
12	11	55.0	11	3 US-09-779-79A-1	Sequence 1, Appli
13	11	55.0	11	3 US-09-93-93-13	Sequence 37, Appli
14	11	55.0	11	3 US-09-935-414-91	Sequence 9, Appli
15	11	55.0	11	3 US-09-886-404-13	Sequence 13, Appli
16	11	55.0	11	3 US-09-805-805-8	Sequence 8, Appli
17	11	55.0	11	3 US-09-821-821-24	Sequence 24, Appli
18	11	55.0	11	3 US-09-893-93-13	Sequence 13, Appli
19	11	55.0	11	3 US-09-935-414-91	Sequence 91, Appli
20	11	55.0	11	3 US-09-867-274-23	Sequence 23, Appli
21	11	55.0	11	3 US-09-935-866-24	Sequence 24, Appli
22	11	55.0	11	3 US-09-928-175-25	Sequence 25, Appli
23	11	55.0	11	3 US-09-995-542-13	Sequence 13, Appli
24	11	55.0	11	3 US-09-987-851-18	Sequence 18, Appli
25	11	55.0	11	3 US-09-984-183-4	Sequence 4, Appli
26	11	55.0	11	3 US-09-949-196-15	Sequence 15, Appli
27	11	55.0	11	3 US-09-948-018-22	Sequence 22, Appli

RESULTS

RESULT 1
US-10-814-109-2
 ; Sequence 2, Application US/10814109
 ; Publication No. US2005222022A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gingrich, Jeffrey
 ; TITLE OF INVENTION: Method for Modification of NMDA Receptors Through Inhibition of
 ; FILE REFERENCE: 2560_004
 ; CURRENT APPLICATION NUMBER: US/10/814,109
 ; CURRENT FILING DATE: 2004-03-30
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 2
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-814-109-2

Query Match Score 100.0%; DB 5; Length 20;
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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRKPPASADGHR 20
 Db 1 YGRKERRQRRKPPASADGHR 20

RESULTS

RESULT 2
US-10-756-774-14
 ; Sequence 14, Application US/10756774
 ; Publication No. US20040156859A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bzrin, Alan M.
 ; TITLE OF INVENTION: PULMONARY DELIVERY FOR BIOCONJUGATION
 ; FILE REFERENCE: 500862001810
 ; CURRENT APPLICATION NUMBER: US/10/756,774
 ; CURRENT FILING DATE: 2004-01-12
 ; PRIOR APPLICATION NUMBER: US 09/656,121
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: US 60/152,681
 ; PRIOR FILING DATE: 1999-09-07
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 14
 ; LENGTH: 12

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; TYPE: PRT ; OTHER INFORMATION: synthetic peptide
; ORGANISM: Artificial Sequence ; US-10-930-192-4
; FEATURE: Peptide ; OTHER INFORMATION: Synthetic Peptide
; US-10-756-774-14 ; Query Match Score 12; DB 4; Length 12;
; Best Local Similarity 100.0%; Pred. No. 0.0001; Indels 0; Gaps 0;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRRK 12
Db 1 YGRKERRQRRRK 12

RESULT 5
US-10-930-192-5
; Sequence 5, Application US/10930192
; Publication No. US20050059597A1
; GENERAL INFORMATION:
; APPLICANT: Tyminski, Michael
; TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
; FILE REFERENCE: 4438 0007
; CURRENT APPLICATION NUMBER: US/10/930,192
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: US 10/208,374
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/584,555
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; US-10-930-192-5

Query Match Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00015; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRRK 12
Db 1 YGRKERRQRRRK 12

RESULT 6
US-10-930-192-12
; Sequence 12, Application US/10930192
; Publication No. US20050059597A1
; GENERAL INFORMATION:
; APPLICANT: Tyminski, Michael
; TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
; FILE REFERENCE: 4438 0007
; CURRENT APPLICATION NUMBER: US/10/930,192
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: US 10/208,374
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/584,555
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; US-10-930-192-12

Query Match Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00015; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRRK 12
Db 1 YGRKERRQRRRK 12

RESULT 4
US-10-930-192-4
; Sequence 4, Application US/10930192
; Publication No. US20050059597A1
; GENERAL INFORMATION:
; APPLICANT: Tyminski, Michael
; TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
; FILE REFERENCE: 4438 0007
; CURRENT APPLICATION NUMBER: US/10/930,192
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: US 10/208,374
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US 09/584,555
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; US-10-930-192-12

Query Match Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00015; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YGRKKRKQRKK 12

RESULT 7
US-11-021-928A-276
; Sequence 276, Application US/11021928A
; Publication No. US20050164933A1
GENERAL INFORMATION:
; APPLICANT: Tyminski, Michael
; APPLICANT: Garman, Jonathan David
; TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
; CURRENT APPLICATION NUMBER: US/11021928A
; FILE REFERENCE: 1889-00800
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 11/021,928A
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 276
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
us-11-021-928A-276

Query Match 60.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRKQRKK 12
Db 1 YGRKKRKQRKK 12

RESULT 8
US-11-021-928A-363
Sequence 363, Application US/11021928A
; Publication No. US20050164933A1
GENERAL INFORMATION:
; APPLICANT: Tyminski, Michael
; APPLICANT: Garman, Jonathan David
; TITLE OF INVENTION: Method of Reducing Injury to Mammalian Cells
; CURRENT APPLICATION NUMBER: US/11021928A
; FILE REFERENCE: 1889-00800
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 11/021,928A
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 363
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
us-11-021-928A-363

Query Match 60.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRKQRKK 12
Db 1 YGRKKRKQRKK 12

RESULT 9
US-11-021-928A-364
; Sequence 364, Application US/11021928A
; Publication No. US20050164933A1

NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence
; FEATURE: NAME/KEY: BINDING
; LOCATION: (22)..(22)
; OTHER INFORMATION: NH2
US-09-949-156-34

Query Match 60.0%; Score 12; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
US-09-815-108-9
; Sequence 9, Application US/09815108
; Patent No. US20020009776A1
; GENERAL INFORMATION:
; APPLICANT: Saris, Christian M.
; APPLICANT: Sharon, Mu X.
; APPLICANT: Xia, Min
; APPLICANT: Boone, Thomas Charles
; APPLICANT: Covey, Todd
; TITLE OF INVENTION: Fibroblast Growth Factor Receptor-Like Molecules and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 99-513-A
; CURRENT APPLICATION NUMBER: US/09/B15,108
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,379
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; US-09-815-108-9

Query Match 55.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15
US-09-815-108-9-13
; Sequence 13, Application US/09886404
; Patent No. US20020037524A1
; GENERAL INFORMATION:
; APPLICANT: Medilock, Eugene
; APPLICANT: Yeh, Richard
; APPLICANT: Slibiger, Scott M.
; APPLICANT: Elliot, Gary S.
; APPLICANT: Nguyen, Hung Q.
; TITLE OF INVENTION: IL-17 Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/37128B
; CURRENT APPLICATION NUMBER: US/09/886,404
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/810,384
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/266,159
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,125
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0

NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-780-070-37

Query Match 55.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
US-09-780-070-37
; Sequence 37, Application US/09780070
; Patent No. US20020009752A1
; GENERAL INFORMATION:
; APPLICANT: Burke, James
; APPLICANT: Strittmatter, Warren
; APPLICANT: Nagai, Yoshitaka
; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE REPEAT
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 5405-242
; CURRENT APPLICATION NUMBER: US/09/780,070
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/189,781
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40

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; SEQ ID NO:13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Peptide of HIV
; OTHER INFORMATION: TAT protein
; OTHER INFORMATION: TAT protein
US-09-886-404-13
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Query Match      55.00;  Score 11;  DB 3;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 0.00086;
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     ||||| | |
Db   1 YGRKKRKQRRL 11
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Title: US-10-814-109-2

Perfect score: 20

Sequence: 1 YGRKRRQRRKPASADGHR 20

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5: /EMC_Celerra_SIDS3/prodata/1/pubpaas/PCT_NEW_PUB_pep;*
6: /EMC_Celerra_SIDS3/prodata/1/pubpaas/US10_NEW_PUB_pep;*
7: /EMC_Celerra_SIDS3/prodata/1/pubpaas/US11_NEW_PUB_pep;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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2	11	55.0	11	6 US-10-547-530-4	Sequence 4, Appli
3	11	55.0	11	6 US-10-559-80A-1	Sequence 1, Appli
4	11	55.0	11	7 US-11-318-535-24	Sequence 24, Appli
5	11	55.0	11	7 US-11-233-610-45	Sequence 45, Appli
6	11	55.0	11	7 US-11-267-986-8	Sequence 8, Appli
7	11	55.0	11	7 US-11-287-817-19	Sequence 19, Appli
8	11	55.0	11	7 US-11-371-285-59	Sequence 59, Appli
9	11	55.0	11	7 US-11-317-804-85	Sequence 85, Appli
10	11	55.0	11	7 US-11-238-034-39	Sequence 39, Appli
11	11	55.0	11	7 US-11-250-830-1	Sequence 1, Appli
12	11	55.0	11	7 US-11-241-836-16	Sequence 16, Appli
13	11	55.0	12	7 US-11-264-074-19	Sequence 19, Appli
14	11	55.0	14	7 US-11-142-051-4	Sequence 4, Appli
15	11	55.0	14	7 US-11-318-535-7	Sequence 7, Appli
16	11	55.0	14	7 US-11-318-535-8	Sequence 8, Appli
17	11	55.0	15	7 US-11-267-986-7	Sequence 7, Appli
18	11	55.0	15	7 US-11-238-035-40	Sequence 40, Appli
19	11	55.0	15	7 US-11-241-836-17	Sequence 19, Appli
20	11	55.0	15	7 US-11-241-836-17	Sequence 17, Appli
21	11	55.0	20	6 US-10-539-677-34	Sequence 34, Appli
22	11	55.0	20	6 US-10-539-677-36	Sequence 36, Appli
23	11	55.0	23	7 US-11-251-952-1	Sequence 1, Appli
24	11	55.0	29	7 US-11-251-734-4	Sequence 4, Appli
25	11	55.0	34	7 US-11-223-610-46	Sequence 46, Appli

ALIGNMENTS

RESULT 1
US-10-547-530-78
; Sequence 78, Application US-10-547-530-78
; Publication No. US20060148086A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of California, The
; Leonard, Rome H.
; APPLICANT: Valerie, Kickhoefer A.
; APPLICANT: Sujana, Ravalos, Fernandes L.
; APPLICANT: Phoebe, Stewart L.
; TITLE OF INVENTION: Vault and vault-like Carrier Molecules
; FILE REFERENCE: 14399-1EP
; CURRENT APPLICATION NUMBER: US-10-547-530
; CURRENT FILING DATE: 2005-08-31
; PRIORITY NUMBER: 60/453,800
; PRIORITY FILING DATE: 2003-03-10
; PRIORITY NUMBER: PCT/US04/07434
; PRIORITY FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 78
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-547-530-78
Query Match 55.0%; Score 11; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Missmatches 0; Indels 0; Gaps 0;
QY 1 YGRKRRQRRR 11
Db 1 YGRKRRQRRR 11

RESULT 2
US-10-518-710-4
; Sequence 4, Application US-10-518-710-4
; GENERAL INFORMATION:
; APPLICANT: Tomizawa, Kazuhito
; APPLICANT: Matsui, Hideki
; TITLE OF INVENTION: Inhibitor of constitutive active forming of carcineurin
; FILE REFERENCE: JP-11650
; CURRENT APPLICATION NUMBER: US-10-518-710-4
; CURRENT FILING DATE: 2004-12-22
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 4

LENGTH: 11
 TYPE: PRT
 ORGANISM: HIV virus
 US-10-518-710-4
 Query Match 55.0%; Score 11; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 APPLICANT: Mizelewski, Gerald J.
 TITLE OF INVENTION: Compositions and Methods of Using Alpha-Peprotein Growth
 FILE REFERENCE: HOLIAND-0516
 CURRENT APPLICATION NUMBER: US/11/223,610
 CURRENT FILING DATE: 2005-09-09
 NUMBER OF SEQ ID NOS: 181
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 45
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-223-610-45

Query Match 55.0%; Score 11; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YGRKKRKQRRL 11
 Db 1 YGRKKRKQRRL 11

RESULT 6
 US-11-267-986-8
 Sequence 8, Application US/11267986
 Publication No. US20060121515A1
 GENERAL INFORMATION:
 APPLICANT: Colamontici, Oscar
 APPLICANT: Siddiqui, Shahnid
 TITLE OF INVENTION: Beta Chain-Associated Regulator of Apoptosis
 FILE REFERENCE: 02-135-D
 CURRENT APPLICATION NUMBER: US/11/267,986
 CURRENT FILING DATE: 2005-11-07
 PRIORITY NUMBER: US 60/359,144
 PRIOR FILING DATE: 2002-02-22
 PRIOR APPLICATION NUMBER: US 10/373,288
 PRIOR FILING DATE: 2003-02-24
 PRIOR APPLICATION NUMBER: US 60/625,745
 PRIOR FILING DATE: 2004-11-05
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 8
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE: OTHER INFORMATION: 11 amino acid protein internalization sequence signal based on t
 OTHER INFORMATION: e HIV tat protein.
 US-11-267-986-8

Query Match 55.0%; Score 11; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 APPLICANT: Karsis, Michael
 TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic
 ACIDS
 FILE REFERENCE: 002877.00028
 CURRENT APPLICATION NUMBER: US/11/318,535
 CURRENT FILING DATE: 2005-12-28
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 24
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus
 US-11-318-535-24

Query Match 55.0%; Score 11; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.6e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 APPLICANT: Lee, Sang-Kyou
 TITLE OF INVENTION: Compositions and Methods of Using Alpha-Peprotein Growth
 FILE REFERENCE: US/112679817
 CURRENT APPLICATION NUMBER: US/112679817
 CURRENT FILING DATE: 2005-09-09
 NUMBER OF SEQ ID NOS: 181
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 46
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-223-610-45

RESULT 7
 US-11-267-817-19
 Sequence 19, Application US/11267817
 Publication No. US20060148060A1
 GENERAL INFORMATION:
 APPLICANT: LEE, SANG-KYOU

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APPLICANT: LEE, SEUNG-KYUO MPH-1-BTM AND THE USE THEREOF
TITLE OF INVENTION: BIOMOLECULE TRANSDUCTION MOTIF MPH-1-BTM AND THE USE THEREOF
FILE REFERENCE: 2435 0010002
CURRENT APPLICATION NUMBER: US/11/267,817
CURRENT FILING DATE: 2005-11-07
PRIOR APPLICATION NUMBER: 10/501,665
PRIOR FILING DATE: 2003-01-20
PRIOR APPLICATION NUMBER: KR 10-2002-0003183
PRIOR FILING DATE: 2002-01-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: KopatentIn 1.71
SEQ ID NO 19
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Protein transduction domain
US-11-267-817-19

Query Match Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YGRKERRQRRR 11
Db 1 YGRKERRQRRR 11

RESULT 8
US-11-271-285-59
Sequence 59 Application US/11271285
Publication No. US20060148700A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Tanaka, Masashi
APPLICANT: Robbins, Robert C.
TITLE OF INVENTION: Methods and Compositions for Reducing Injury to a Transplant
FILE REFERENCE: 58600-8218 US00
CURRENT APPLICATION NUMBER: US/11/271,285
CURRENT FILING DATE: 2005-11-10
PRIOR APPLICATION NUMBER: US 60/626,564
PRIOR FILING DATE: 2004-11-10
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.3
SEQ ID NO 59
LENGTH: 11
TYPE: PRT
ORGANISM: Human immunodeficiency virus 1
US-11-271-285-59

Query Match Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YGRKERRQRRR 11
Db 1 YGRKERRQRRR 11

RESULT 9
US-11-317-806-85
Sequence 85 Application US/11317806
Publication No. US20060148702A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Bright, Rachel
TITLE OF INVENTION: Methods of Increasing Cerebral Blood Flow
FILE REFERENCE: 58600-8214 US00
CURRENT APPLICATION NUMBER: US/11/317,806
CURRENT FILING DATE: 2005-12-23
PRIOR APPLICATION NUMBER: US 60/641,413
PRIOR FILING DATE: 2005-01-04

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; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 85
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus 1
US-11-317-806-85

Query Match      55 0%; Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 YGRKKRKQRRL 11
Db          1 YGRKKRKQRRL 11

RESULT 10
US-11-238-035-39
; Sequence 39, Application US/11238035
; Publication No. US20060160181A1
; GENERAL INFORMATION:
;   APPLICANT: Luetky, Roland
;   APPLICANT: Yang, Robert
;   APPLICANT: Suggs, Sidney V.
;   APPLICANT: Sarosi, Ildiko
; TITLE OF INVENTION: Fibroblast Growth Factor-23 Molecules and Uses Thereof
; FILE REFERENCE: 01-004
; CURRENT APPLICATION NUMBER: US/11/238,035
; NUMBER OF SEQ ID NOS: 54
; CURRENT FILING DATE: 2005-09-28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 39
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-238-035-39

Query Match      55 0%; Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 YGRKKRKQRRL 11
Db          1 YGRKKRKQRRL 11

RESULT 11
US-11-250-830-1
; Sequence 1, Application US/11250830
; Publication No. US20060159619A1
; GENERAL INFORMATION:
;   APPLICANT: BECKER, MATTHEW L.
;   APPLICANT: FANG, HUAENG
;   APPLICANT: LI, XIAOKU
;   APPLICANT: PAN, DIPIANJAN
;   APPLICANT: ROSSIN, RAFFAELLA
;   APPLICANT: SUN, XIANKAI
;   APPLICANT: TAYLOR, JOHN-STEPHEN
;   APPLICANT: TURNER, JEFFREY L.
;   APPLICANT: WELCH, MICHAEL JOHN
;   APPLICANT: WOOLLEY, KAREN L.
; TITLE OF INVENTION: CELL-PERMEABLE NANOCONJUGATES OF SHELL-CROSSLINKED
; TITLE OF INVENTION: KNEDEL (SCK) AND PEPTIDE NUCLEIC ACIDS ("PNAs") WITH
; TITLE OF INVENTION: UNIQUELY EXPRESSED OR OVER-EXPRESSED mRNA TARGETING
; TITLE OF INVENTION: SEQUENCES FOR EARLY DIAGNOSIS AND THERAPY OF CANCER
; FILE REFERENCE: 15060-75
; CURRENT APPLICATION NUMBER: US/11/250,830
; CURRENT FILING DATE: 2005-10-14
; PRIOR APPLICATION NUMBER: 60/619,242
; PRIORITY FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 3.1

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SEQ ID NO: 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-11-250-830-1

Query Match Score 11; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.6e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKRRQRQQ 11
Db 1 YGRKRRQRQQ 11

RESULT 14
US-11-142-051-4
; Sequence 4, Application US/11142051
; Publication No. US20061010956A1
; GENERAL INFORMATION:
; APPLICANT: Pincus, Matthew
; APPLICANT: Michl, Josef
; TITLE OF INVENTION: PHENOTYPIC REVERSION OF PANCREATIC CARCINOMA CELLS
; FILE REFERENCE: 1181-26
; CURRENT APPLICATION NUMBER: US/11/142,051
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US 60/575,131
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: US 60/575,846
; PRIOR FILING DATE: 2004-05-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
SEQ ID NO: 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide; HIV-1 TAT membrane penetrating sequence
US-11-142-051-4

Query Match 55.0%; Score 11; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKRRQRQQ 11
Db 1 YGRKRRQRQQ 11

RESULT 15
US-11-318-535-7
; Sequence 7, Application US/11318535
; Publication No. US2006106197A1
; GENERAL INFORMATION:
; APPLICANT: Karab, Michael
; TITLE OF INVENTION: Intracellular Delivery of Small Molecules, Proteins, and Nucleic
; ACIDS
; FILE REFERENCE: 002877_00028
; CURRENT APPLICATION NUMBER: US/11/318,535
; CURRENT FILING DATE: 2005-12-28
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
SEQ ID NO: 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: protein transduction domain
; NAME/KEY: MIS-C FEATURE
; LOCATION: (1).-(1)
; OTHER INFORMATION: Biotin
US-11-318-535-7

Query Match 55.0%; Score 11; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKRRQRQQ 11
Db 4 YGRKRRQRQQ 14

RESULT 13
US-11-264-074-19
; Sequence 19, Application US/11264074
; Publication No. US20061048104A1
; GENERAL INFORMATION:
; APPLICANT: Marini, et al.
; TITLE OF INVENTION: Detection and Ion Channel or Receptor Activity
; FILE REFERENCE: 0492611-0647
; CURRENT APPLICATION NUMBER: US/11/264,074
; CURRENT FILING DATE: 2005-10-31
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.2
SEQ ID NO: 19
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: TAT peptide
US-11-264-074-19

Query Match 55.0%; Score 11; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 32 secs

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OM protein - protein search, using sw model

Run on: August 24, 2006 23:46:43 ; Search time 38 Seconds (without alignments)

50.640 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 20

Sequence: 1 YGRKRRQRRKPSADGHR 20

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs., 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80;*

- 1: pir1;*
- 2: pir2;*
- 3: pir3;*
- 4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	55.0	71	2 T09384	trans-activating t
2	11	55.0	72	1 TNLJH4	trans-activating t
3	11	55.0	86	1 TNLJZR	trans-activating t
4	11	55.0	86	2 A25700	trans-activating t
5	11	55.0	86	2 JC5591	trans-activator pro
6	11	55.0	86	2 S53181	tat protein - huma
7	11	55.0	86	2 S33382	trans-activating t
8	11	55.0	87	2 T01665	tat protein - huma
9	11	55.0	95	1 TNLJ12	trans-activating t
10	11	55.0	101	1 E4001	trans-activating t
11	11	55.0	101	2 T09446	tat protein - huma
12	10	50.0	86	1 TNLJND	trans-activating t
13	9	45.0	541	1 A43610	protein-tyrosine K
14	9	45.0	542	1 TVRUSC	probable pilin Ngr
15	7	35.0	143	2 AE2781	hypothetical prote
16	7	35.0	668	2 T29884	hypothetical prote
17	7	35.0	1951	2 S00320	sodium channel pro
18	7	35.0	1983	2 A60054	riboosomal protein
19	6	30.0	29	2 S08355	probable 50S ribos
20	6	30.0	46	2 AI0560	probable pilin Ngr
21	6	30.0	53	4 S15048	hypothetical prote
22	6	30.0	78	2 E97064	NO! protein, nitra
23	6	30.0	80	2 T01320	hypothetical prote
24	6	30.0	80	2 C95994	transport protein
25	6	30.0	81	2 T47865	trans-activating t
26	6	30.0	100	1 TNLJSI	trans-regulatory s
27	6	30.0	103	1 VKLJGG	trans-regulatory s
28	6	30.0	108	2 VKLJS2	vira/G regulated p
29	6	30.0	108	2 AI3250	

ALIGNMENTS

RESULT 1
T09384
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Dec-2004
C;Accession: T09384
R;Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.; Bir
J. Virol. 69, 4228-4236, 1995
A;Title: Defective accessory genes in a human immunodeficiency virus type 1-infected lar
A;Reference number: Z16654; PMID: 9287475; PMID: 7769682
A;Accession: T09384
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-71 <MIC>
A;Cross-references: UNIPROT:Q71926; UNIPARC:UPI00000FF00C; EMBL:U24451; NID:g829440; PI
C;Genetics:
A;Gene: tat
C;Superfamily: leukemia virus trans-activating transcription regulator
C;Keywords: transcription

Query Match 55.0%; Score 11; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKERRQRR 11
Db 47 YGRKERRQRR 57

RESULT 2
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trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004
C;Accession: B25523
R;Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare,
Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986
A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human
A;Reference number: A94136; PMID: 87041461; PMID: 3490666
A;Accession: B25523
A;Molecule type: DNA
A;Residues: 1-72 <DE5>
A;Cross-references: UNIPARC:UPI000174A5; GB:MI1337; NID:g126460
A;Note: the GenBank entry ADRE3AA PID:g209908 differs from the published sequence in tra
C;Genetics:
A;Gene: tat
C;Superfamily: transcription regulation
C;Keywords: transcription

Query Match 55.0%; Score 11; DB 1; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 11; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A;Residues: 1-86 <H02>
 A;Cross-references: UNIPARC:UPI000017865E
 C;Comment: This protein is a key regulatory protein in the viral replication cycle and b
 C;Superfamily: leukemia virus trans-activating transcription regulator
 P;22-31/Region: cysteine-rich

Query Match Score 11; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A;Residues: 1-86 <H02>
 A;Cross-references: UNIPARC:UPI000017865E
 C;Species: human immunodeficiency virus type 1
 C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 31-Dec-2004
 C;Accession: C26192
 R;Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Schochetman, G.; Cu
 Gene 52, 71-82, 1987
 A;Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleot
 A;Reference number: A26192; MUID:87248097; PMID:3036660
 A;Accession: C26192
 A;Molecule type: DNA
 A;Residues: 1-86 <SRI>
 A;Cross-references: UNIPROT:PO4609; UNIPARC:UPI000013693A; GB:K03458; GB:M16322; NID:932
 A;Gene: tat
 A;Introns: 72/3
 C;Superfamily: leukemia virus trans-activating transcription regulator
 C;Keywords: AIDS; immunodeficiency; transcription regulation

Query Match Score 11; DB 1; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A;Residues: 1-86 <H02>
 A;Cross-references: UNIPARC:UPI000013693A; GB:K03458; GB:M16322; NID:932
 C;Species: human immunodeficiency virus type 1
 C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 31-Dec-2004
 C;Accession: C26192
 R;Sodroski, J.; Patarca, R.; Rosen, C.; Wong-Staal, F.; Haseltine, W.
 Science 229, 74-77, 1985
 A;Reference number: A25700; MUID:85244627; PMID:2990041
 A;Accession: A25700
 A;Status: Preliminary
 A;Molecule type: mRNA
 A;Residues: 1-86 <SOD>
 A;Cross-references: UNIPROT:PO4610; UNIPARC:UPI0000111F40
 C;Superfamily: leukemia virus trans-activating transcription regulator

Query Match Score 11; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A;Residues: 1-86 <H02>
 A;Cross-references: UNIPARC:UPI000000419; EMBL:Z11530; NID:960192; PIDN
 C;Species: human immunodeficiency virus type 1
 C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 31-Dec-2004
 C;Accession: JC5591
 R;Hoffmann, S.; Willbold, D.
 Biochem. Biophys. Res. Commun. 235, 806-811, 1997
 A;Title: A selection system to study protein-RNA interactions: Functional display of HIV
 A;Reference number: JC5591; MUID:97350867; PMID:9207243
 A;Accession: JC5591
 A;Molecule type: protein

Query Match Score 11; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 Query Match Score 11; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A;Residues: 1-86 <H02>
 A;Cross-references: UNIPARC:UPI000013693B; EMBL:M22639; NID:9329377; PIDN
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 31-Dec-2004
 C;Accession: S54381
 R;Theodore, T.; Buckler-White, A.J.
 submitted to the EMBL Data Library, July 1989
 A;Reference number: S54381
 A;Accession: S54381
 A;Status: preliminary
 A;Molecule type: genomic RNA
 A;Residues: 1-86 <THB>
 A;Cross-references: UNIPROT:P12506; UNIPARC:UPI000013693B
 C;Genetics:
 A;Introns: 72/2
 C;Superfamily: leukemia virus trans-activating transcription regulator

Query Match Score 11; DB 2; Length 86;
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 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A;Residues: 1-86 <H02>
 A;Cross-references: UNIPARC:UPI000013693B; EMBL:M22639; NID:9329377; PIDN
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 31-Dec-2004
 C;Accession: S54382
 R;Carlini, F.
 submitted to the EMBL Data Library, November 1991
 A;Reference number: S33979
 A;Accession: S33982
 A;Molecule type: DNA
 A;Residues: 1-86 <CAR>
 A;Cross-references: UNIPROT:P04606; UNIPARC:UPI0000000419; EMBL:Z11530; NID:960192; PIDN
 R;Iderovski, D.P.; Matsuyama, T.; Frigerio, B.; Chui, S.; Min, X.; Erie, H.; Sumner-Su
 Nucleic Acids Res. 20, 5311-5320, 1992
 A;Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activator
 A;Reference number: S26385
 A;Accession: S26385
 A;Molecule type: nucleic acid
 A;Residues: 1-86 <SID>
 A;Cross-references: UNIPARC:UPI000000419; EMBL:X64650; NID:960144; PIDN:CAA45921.1; PI
 C;Genetics:
 A;Gene: tat
 A;Introns: 72/2
 C;Superfamily: leukemia virus trans-activating transcription regulator

Query Match Score 11; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 Query Match Score 11; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.00039;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
Db 47 YGRKKRQRRR 57

RESULT 8
T01665
tat protein - human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Accession: T01665
R;Allison, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isolates
A;Reference number: Z14389; MUID:86245056; PMID:2424612
A;Accession: T01665
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-87 <Ali>
A;Cross-references: UNIPROT:PO4613; UNIPARC:UPI00001132A9; EMBL:K03456; NID:g60228; PIDN
C;Genetics:
A;Introns: 72/2
C;Superfamily: leukemia virus trans-activating transcription regulator

Query Match 55.0%; Score 11; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
Db 47 YGRKKRQRRR 57

RESULT 9
TNLJ12
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Accession: A04017
R;Arya, S.K.; Gallo, R.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986
A;Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity of
A;Reference number: A94093; MUID:86177573; PMID:3008154
A;Accession: A04017
A;Molecule type: DNA
A;Residues: 1-95 <ARY>
A;Cross-references: UNIPROT:PO4326; UNIPARC:UPI0000174A54
C;Genetics:
A;Gene: tat
C;Superfamily: leukemia virus trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 55.0%; Score 11; DB 1; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
Db 56 YGRKKRQRRR 66

RESULT 10
E44001
trans-activating transcription regulator - human immunodeficiency virus type 1 (strain Y
N;Alternate names: tat protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Accession: E44001
R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6590, 1992
A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; MUID:93021387; PMID:1404605
A;Accession: E44001
A;Molecule type: DNA
A;Cross-references: UNIPROT:P35965; UNIPARC:UPI0000136937; GB:M93258
C;Genetics:
A;Gene: tat
A;Introns: 72/2
C;Keywords: AIDS; immunodeficiency; transcription regulation
C;Species: leukemia virus trans-activating transcription regulator

Query Match 55.0%; Score 11; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 11
Db 47 YGRKKRQRRR 57

RESULT 11
T09446
tat protein - human immunodeficiency virus type 1 (strain JRFL)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004
C;Accession: T09446
R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitted to the EMBL Data Library, July 1996
A;Reference number: Z16673
A;Accession: T09446
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-101 <PAN>
A;Cross-references: UNIPROT:Q75758; UNIPARC:UPI0000109776; EMBL:U63632; NID:g1465777; EMBL:U63632; NID:91465777; PI

RESULT 12
TNLJND
trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Accession: JQ0071
R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A., Gene 81, 275-284, 1989
A;Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immunodeficiency virus
A;Reference number: JQ0071
A;Accession: JQ0071
A;Molecule type: DNA
A;Residues: 1-86 <SP1>
A;Cross-references: UNIPROT:P18804; UNIPARC:UPI00001AD5D6; GB:M27323; NID:9328154; PIDN:
C;Genetics:
A;Gene: tat
C;Superfamily: leukemia virus trans-activating transcription regulator
C;Keywords: AIDS; immunodeficiency; transcription

Query Match 50.0%; Score 10; DB 1; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRR 10

Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy	5 KRRQRR 11
Db	41 KRRQRR 47

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Job time : 40 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.9	Q5ug48 human immun
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on: August 24, 2006, 23:43:13 ; Search time 300 Seconds (without alignments) 61.668 Million cell updates/sec		Q5ug53 human immun
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effect score: 20		Q5ug55 human immun
quence: 1 YCRKCRQRKKPASADGHR 20		Q5ug56 human immun
oring table: OLIGO	Gapext 60.0 , Gapext 60.0	Q5ug57 human immun
searched: 2849598 seqs, 925015592 residues		Q5ug58 human immun
size : 1		Q5ug59 human immun
al number of hits satisfying chosen parameters:	2849579	Q5ug60 human immun
DB seq length: 0		Q5ug61 human immun
imum DB seq length: 2000000000		Q5ug62 human immun
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base : UniProt 7.2.*		Q5ug64 human immun
1: uniprot_sprot;*		Q5ug65 human immun
2: uniprot_trembl;*		
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES		
#	Query	Description
hit no.	Score	Match Length DB ID
1	12	Q6Y0V6 9HIV1
2	11	TAT HIV1B5
3	11	Q6AV2 9HIV1
4	11	Q75544 9HIV1
5	11	Q75544 9HIV1
6	11	Q6QAV4 9HIV1
7	11	Q66MQ1 9HIV1
8	11	Q40224 9HIV1
9	11	Q40225 9HIV1
10	11	Q40226 9HIV1
11	11	Q40227 9HIV1
12	11	Q40228 9HIV1
13	11	Q40231 9HIV1
14	11	Q40232 9HIV1
15	11	Q40233 9HIV1
16	11	Q40234 9HIV1
17	11	Q3S9T9 9HIV1
18	11	Q3S9U 9HIV1
19	11	Q3S9W0 9HIV1
20	11	Q3S9W8 9HIV1
21	11	Q5BPY1 9HIV1
22	11	Q58Q03 9HIV1
23	11	Q58Q10 9HIV1
24	11	Q58Q64 9HIV1
25	11	Q58Q69 9HIV1
26	11	Q5G7E5 9HIV1
27	11	Q5UG44 9HIV1
28	11	Q5UG45 9HIV1
29	11	Q5UG52 9HIV1
30	11	Q5UG46 9HIV1
31	11	Q5UG47 9HIV1
32	11	Q5UG48 9HIV1
33	11	Q5UG50 9HIV1
34	11	Q5UG51 9HIV1
35	11	Q5UG52 9HIV1
36	11	Q5UG53 9HIV1
37	11	Q5UG54 9HIV1
38	11	Q5UG55 9HIV1
39	11	Q5UG56 9HIV1
40	11	Q5UG57 9HIV1
41	11	Q5UG58 9HIV1
42	11	Q5UG59 9HIV1
43	11	Q5UG60 9HIV1
44	11	Q5UG61 9HIV1
45	11	Q5UG62 9HIV1
		Q5UG63 9HIV1
		Q5UG64 9HIV1
		Q5UG65 9HIV1
		ALIGMENTS
RESULT 1		
Q6Y0V6_9HIV1		
ID Q6Y0V6_9HIV1		PRELIMINARY;
AC Q6Y0V6;		PRT;
DT 05-JUL-2004,		86 AA.
DT 05-JUL-2004,		integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006		sequence version 1.
DE Tat protein (Fragment).		
GN Name=tat;		
OS Human immunodeficiency virus 1.		
Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;		
OC Lentivirus; Primate lentivirus group.		
OX NCBI_TaxID=11676;		
RN [1] _		
RP NUCLEOTIDE SEQUENCE.		
RX MEDLINE=22912857; PubMed=14518888; DOI=10.1086/378412;		
RG The Tat Multicentric Study Group, Ruiz-Alvarez M.J., Scoglio A.,		
Butto S., Fiorelli V., Tripiciano A., Ruijter M.J., Sabbatucci M., Cafaro A.,		
Guzman C.A., Borsetti A., Caputo A., Vardas E., Colvin M., Lukwya M.,		
Rezza G., Enzoli B.;		
RT "Sequence Conservation and Antibody Cross-Recognition of Clade B Human Immunodeficiency Virus (HIV), Type 1 Tat Protein in HIV-1-Infected RT		
RT Italians, Ugandans, and South Africans.",		
RL J. Infect. Dis. 188: 1171-1180 (2003).		
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CC		
DR EMBL; AT19398; AAP33727.1; -; Genomic_DNA		
DR HSSP; P04613; 1K5K;		
DR GO; P04205; C: host cell nucleus; IEA.		
DR GO; GO:0005634; C:nucleus; IEA.		
DR GO; GO:0003733; F:RNA binding; IEA.		
DR GO; GO:0003700; P:transcription factor activity; IEA.		
DR GO; GO:0006355; P:transcription of transcription, DNA-dependent; IEA.		
DR GO; GO:0006350; P:transcription; IEA.		
DR Interpro; IPR00181; IV_Rat.		
DR Pfam; PF00539; Tat; 1; PRNTS; PR00055; HIVtDOMAIN		
KW Activator; Nuclear protein; RNA-binding; Transcription		
KW Transcription regulation.		
FT NON_TER	86	
SQ SEQUENCE	86 AA;	9840 MW; AD27037029ACAOEA CRC64;
Query Match	60.0%	Score 12; DB 2; Length 86;
Best Local Similarity	100.0%	Pred. No. 0.0011;
Matches 12;	Conservative 0;	Mismatches 0;
Indels 0;	Gaps 0;	
Qy 1 YGRKRRQRPRRK 12		
Db 47 YGRKRRQRPRRK 58		

RESULT 2															
TAT_HV1B5	STANDARD;	PRT;	58 AA.	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms											
ID P04612;	Distributed under the Creative Commons Attribution-NoDerivs License														
DT 13-AUG-1987; integrated into UniProtKB/Swiss-Prot.															
DT 07-FEB-2006, entry version 40.															
DE TAT protein (transactivating regulatory protein) (Fragment).															
DE Name=stat;															
DS Human immunodeficiency virus type 1 (isolate BH5) (HIV-1).															
DOC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;															
DOC Lentivirus; Primate lentivirus group.															
NCBI_TaxID=11682;															
RN NUCLEOTIDE SEQUENCE [GENOMIC RNA].	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms														
RX MEDLINE=5111123; Published=2578615;	Distributed under the Creative Commons Attribution-NoDerivs License														
RA Ratner L., Haseltine W.A., Patarca R., Livak K.J., Starcich B.R.,															
RA Joseph S.P., Doran E.P., Baumeister K., Ivanoff L., Baumeister J.A., Whitehorn E.A., Whithorn E.A.,															
RA Baumeister K., Ivanoff L., Peteway S.R. Jr., Pearson M.L., Pearson M.L., Jr.,															
RA Lautenberger J.A., Papas T.S., Gharayeb J., Chang N.T., Gallo R.C.,															
RA Wong-Staal F.,															
RT "Complete nucleotide sequence of the AIDS virus, HIV-1II.";															
RL Nature 313:277-278 (1985).															
CC -1- FUNCTION: Transcriptional regulator that acts by binding to the trans-activating responsive sequence (TAR) RNA element and activates transcription initiation and/or elongation from the LTR promoter.															
CC -1- SUBCELLULAR LOCATION: Nucleus; nucleolar.															
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DR EMBL; P04610; 1JFW.	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms														
DR HSSP; P04612; 1-47.	Distributed under the Creative Commons Attribution-NoDerivs License														
DR HIV; K02012; TAT\$BH5.															
DR InterPro; IPR001831; IV_Tat.															
DR Pfam; PF00539; Tat_1.															
DR PRINTS; PRO0055; HIV\$TDOMAIN.															
KW Activator; AIDS; Nuclear protein; RNA-binding; Transcription; Transcription regulation.	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms														
KW FT TAT protein.	Distributed under the Creative Commons Attribution-NoDerivs License														
FT >58 /FTId=PRO_0000085343.															
FT NON_TER	58 AA;	6800 MW;	E36C21F8FFD813E3 CRC64;	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms											
FT SEQUENCE	58 AA;	6800 MW;	E36C21F8FFD813E3 CRC64;	Distributed under the Creative Commons Attribution-NoDerivs License											
FT	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms														
FT Score 55.0%; Length 58;	Distributed under the Creative Commons Attribution-NoDerivs License														
FT Best Local Similarity 100.0%; Pred. No. 0.00083;															
FT Matches 0;	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms														
FT Indels 0;	Distributed under the Creative Commons Attribution-NoDerivs License														
FT Gaps 0;															
FT	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms														
FT Score 55.0%; Length 65;	Distributed under the Creative Commons Attribution-NoDerivs License														
FT Best Local Similarity 100.0%; Pred. No. 0.00092;															
FT Matches 0;	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms														
FT Indels 0;	Distributed under the Creative Commons Attribution-NoDerivs License														
FT Gaps 0;															
RESULT 3	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms														
Q6QAV2_9HIV1	PRELIMINARY;	PRT;	64 AA.	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms											
Q6QAV2_9HIV1	PRELIMINARY;	PRT;	64 AA.	Distributed under the Creative Commons Attribution-NoDerivs License											
Q6QAV2_9HIV1	PRELIMINARY;	PRT;	64 AA.	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms											
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Q6QAV2_9HIV1	PRELIMINARY;	PRT;	64 AA.	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms											
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Q6QAV2_9HIV1	PRELIMINARY;	PRT;	64 AA.	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms											
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Q6QAV2_9HIV1	PRELIMINARY;	PRT;	64 AA.	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms											
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Q6QAV2_9HIV1	PRELIMINARY;	PRT;	64 AA.	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms											

Qy	1 YGRKKRQRRR 11	CC	Distributed under the Creative Commons Attribution-NoDerivs License
Db	47 YGRKKRQRRR 57	CC	EMBL; AY549942; AAS67916.1; -; Genomic_DNA.
RESULT 5		DR	SMR; Q6QAV4; 1-68.
ID Q75544_9HIV1	PRELIMINARY; PRT; 65 AA.	DR	GO; GO:0042025; C:host cell nucleus; IEA.
AC Q75544;		DR	GO; GO:005634; C:nucleus; IEA.
DT 01-NOV-1996, integrated into UniProtKB/T-EMBL.		DR	GO; GO:003723; F:RNA binding; IEA.
DT 01-NOV-1996, sequence version 1.		DR	GO; GO:006350; P:transcription factor activity; IEA.
DT 07-FEB-2006, entry version 26.		DR	GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
DT Tat protein (Fragment).		DR	InterPro; IPR01831; IV_Tat.
GN Name=rat.		DR	Pfam; PF00539; Tat; 1.
OS Human immunodeficiency virus 1.		DR	PRINTS; PR00055; HIVTATDOMAIN.
OC Lentivirus; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;		KW	Activator; Nuclear protein; RNA-binding; Transcription; Transcription regulation.
OX NCBI_TaxID=11676;		FT	KW
RN [1]		NON_TER	1 1
RP NUCLEOTIDE SEQUENCE.		SEQUENCE	55 AA; 7983 MW; 326A05D50078CD29 CRC64;
RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;		Best_Local_Similarity	100.0%; Pred. No. 0.00095;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.		Matches	0; Mismatches 0; Indels 0; Gaps 0;
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		Qy	1 YGRKKRQRRR 11
CC Distributed under the Creative Commons Attribution-NoDerivs License		Db	
CC		43 YGRKKRQRRR 53	
DR EMBL; U57252; ARB17812.1; -; Genomic_DNA.		RESULT 7	
DR HSSP; P12506; ITPC.		ID Q66MQ1_9HIV1	Score 11; DB 2; Length 68;
DR GO; GO:0042025; C:host cell nucleus; IEA.		ID Q66MQ1_9HIV1	PRELIMINARY; PRT; 70 AA.
DR GO; GO:005634; C:nucleus; IEA.		AC Q66MQ1;	
DR GO; GO:003723; F:RNA binding; IEA.		DT 11-OCT-2004, integrated into UniProtKB/TREMBL.	
DR GO; GO:0003700; F:transcription factor activity; IEA.		DT 11-OCT-2004, sequence version 1.	
DR GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.		DT 07-FEB-2006, entry version 8.	
DR InterPro; IPR001831; IV_Tat.		DE Tat protein (Fragment).	
DR Pfam; PF00539; Tat; 1.		GN Name=rat;	
DR PRINTS; PR00055; HIVTATDOMAIN.		OS Human immunodeficiency virus 1.	
KW Activator; Nuclear protein; RNA-binding; Transcription; Transcription regulation.		OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; Lentivirus; Primate lentivirus group.	
FT NON_TER	1 1	OX NCBITaxonID=11676;	
SQ SEQUENCE 65 AA; 7677 MW; 91584F861F6A8362 CRC64;		RN [1]	
Query Match 55.0%; Score 11; DB 2; Length 65;		RP NUCLEOTIDE_SEQUENCE.	
Best Local Similarity 100.0%; Pred. No. 0.00092;		RA Herring B.L., Grant R.M., Delwart E.L.; RT "No superinfection among seroconcordant couples after well-defined RT exposure.",	
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.	
Qy 1 YGRKKRQRRR 11		CC CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Db 47 YGRKKRQRRR 57		CC CC	Distributed under the Creative Commons Attribution-NoDerivs License
RESULT 6		DR EMBL; AY666119; AU005440.1; -; Genomic_RNA.	
ID Q6QAV4_9HIV1	PRELIMINARY; PRT; 68 AA.	DR	SMR; Q66MQ1; 1-70.
AC Q6QAV4;		DR	GO; GO:0042025; C:host cell nucleus; IEA.
DT 05-JUL-2004, integrated into UniProtKB/TREMBL.		DR	GO; GO:005634; C:nucleus; IEA.
DT 05-JUL-2004, sequence version 1.		DR	GO; GO:003723; F:RNA binding; IEA.
DT 07-FEB-2006, entry version 10.		DR	GO; GO:0003700; F:transcription factor activity; IEA.
DB Tat protein (Fragment).		DR	GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.
GN Name=rat.		DR	InterPro; IPR01831; IV_Tat.
OS Human immunodeficiency virus 1.		DR	Pfam; PF00539; Tat; 1.
OC Lentivirus; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;		DR	PRINTS; PR00055; HIVTATDOMAIN.
OC Lentivirus; Primate lentivirus group.		KW Activator; Nuclear protein; RNA-binding; Transcription; Transcription regulation.	
OX NCBI_TaxID=11676;		FT NON_TER	70 70 AA; 8096 MW; 28E39B5672863DBB CRC64;
RN [1]		SQ SEQUENCE	
RP NUCLEOTIDE_SEQUENCE.		Query Match 55.0%; Score 11; DB 2; Length 70;	
RX PubMed=1517352; DOI=10.1089/08892204323048087;		Best_Local_Similarity 100.0%; Pred. No. 0.00098;	
RA Andreo S.M.S., Barra L.A.C., Costa L.J., Sucupira M.C.A., Souza I.E.L., Diaz R.S.;		Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
"HIV Type I Transmission by Human Bite."		Qy 1 YGRKKRQRRR 11	
RL AIDS Res. Hum. Retroviruses 20:349-350 (2004).		Db 47 YGRKKRQRRR 57	
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PRINTS: PR00055; HIVATDOMAIN.	DT 01-JAN-1998; sequence version 1.
KW Activator; Nuclear protein; RNA-binding; Transcription.	DT 07-FEB-2006, entry version 25.
KW Transcription regulation.	DE Tat protein (Fragment).
FT NON_TER 71 71	GN Name=rat;
SQ SEQUENCE 71 AA; 8337 MN; 50BB96328495EEA2C CRC64;	OS Human immunodeficiency virus 1.
Query Match Score 11; DB 2; Length 71;	OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
Best Local Similarity 100.0%; Pred. No. 0.00099;	OC Lentivirus; Primate lentivirus group.
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OX NCBITaxID=11676;
Qy 1 YGRKKRQRRR 11	RN [1]
Db 47 YGRKKRQRRR 57	RP NUCLEOTIDE SEQUENCE.
RESULT 11	RT STRAIN=H93-A1cat;
ID O40227_9HIV1 PRELIMINARY; PRT; 71 AA.	RC MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
AC	RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L., Desrosiers R.C.;
DT 01-JAN-1998, integrated into UniProtKB/TREMBL.	RA "Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat1 genes derived from individuals with different rates of disease progression." Virology 232:319-331(1997).
DT 01-JAN-1998, sequence version 1.	CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License.
DT 07-FEB-2006, entry version 25.	CC
DE Tat protein (Fragment).	CC EMBL; AP000526; AAB62525.1; -; Genomic_DNA.
GN Name=rat;	DR HSSP; P04610; 1JFW.
OS Human immunodeficiency virus 1.	DR SMR; O40228; 1-71.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;	DR GO; GO:0043225; C:host cell nucleus; IEA.
OC Lentivirus; Primate lentivirus group.	DR GO; GO:005634; C:nucleus; IEA.
OX NCBITaxID=11676;	DR PRINTS; PF003723; F:RNA binding; IEA.
RN [1]	DR GO; GO:0003700; P:transcription factor activity; IEA.
RP NUCLEOTIDE SEQUENCE.	DR GO; GO:0006350; P:transcription of transcription, DNA-dependent; IEA.
RC STRAIN=CH9-A279;	DR InterPro; IPR001831; IV_Tat.
RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L., Desrosiers R.C.;	DR Pfam; PF00539; Tat; 1.
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat1 genes derived from individuals with different rates of disease progression." Virology 232:319-331(1997).	DR PRINTS; PR00055; HIVATDOMAIN Activator; Nuclear protein; RNA-binding; Transcription; Transcription regulation.
RT NON_TER 71 71	FT NON_TER 71 AA; 8191 MW; C880034AEAFF30E5 CRC64;
RL HSSP; P04610; 1JFW.	CC Query Match Score 11; DB 2; Length 71;
DR HSSP; P04610; 1JFW.	CC Best Local Similarity 100.0%; Pred. No. 0.00099;
DR HSSP; P04610; 1JFW.	CC Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR SMR; O40227; 1-71.	Qy 1 YGRKKRQRRR 11
DR GO; GO:0042025; C:host cell nucleus; IEA.	Db 47 YGRKKRQRRR 57
DR GO; GO:0005634; C:nucleus; IEA.	RESULT 13
DR GO; GO:0003723; F:RNA binding; IEA.	ID O40231_9HIV1 PRELIMINARY; PRT; 71 AA.
DR GO; GO:0003700; F:transcription factor activity; IEA.	AC O40231;
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.	DT 01-JAN-1998, integrated into UniProtKB/TREMBL.
DR GO; GO:0005350; P:transcription; IEA.	DT 01-JAN-1998, sequence version 1.
DR GO; GO:0005350; P:transcription; IEA.	DT 07-FEB-2006, entry version 25.
DR Pfam; PF000539; Tat; 1.	DE Tat protein (Fragment).
DR PRINTS; PR00055; HIVATDOMAIN.	GN Name=rat;
KW Activator; Nuclear protein; RNA-binding; Transcription;	OS Human immunodeficiency virus 1.
KW Transcription regulation.	OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
FT NON_TER 71 71	OC Lentivirus; Primate lentivirus group.
SQ SEQUENCE 71 AA; 8247 MW; C880B05C90230E5 CRC64;	OX NCBITaxID=11676;
Query Match Score 11; DB 2; Length 71;	RP NUCLEOTIDE SEQUENCE.
Best Local Similarity 100.0%; Pred. No. 0.00099;	RC STRAIN=H93-A1cat;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RC MEDLINE=97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;
Qy 1 YGRKKRQRRR 11	RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L., Desrosiers R.C.;
Db 47 YGRKKRQRRR 57	RA "Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat1 genes derived from individuals with different rates of disease progression." Virology 232:319-331(1997).
RESULT 12	CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
O4 0228_9HIV1 PRELIMINARY; PRT; 71 AA.	DT
AC 040228_9HIV1 PRELIMINARY; PRT; 71 AA.	RT
DT 01-JAN-1998, integrated into UniProtKB/TREMBL.	RL

Distributed under the Creative Commons Attribution-NoDerivs License									
<hr/>									
CC	EMBL; AF00529; AAB2528.1; - ; Genomic_DNA.	Matches	11;	Conservative	0;	Mismatches	0;	Indels	0;
CC	HSSP; P04110; 1JFW.	Qy	1 YGRKKRQRRL 11 						
DR	GO; CO:002025; C:host cell nucleus; IEA.	Db	47 YGRKKRQRRL 57						
DR	GO; GO:005634; C:nucleus; IEA.	RESULT 15							
DR	GO; GO:003723; F:RNA binding; IEA.	ID	O40233_9HIV1	PRELIMINARY;	PRT;	71 AA.			
DR	GO; GO:003700; F:transcription factor activity; IEA.	ID	O40233_9HIV1	PRELIMINARY;	PRT;	71 AA.			
DR	GO; GO:006355; P:regulation of transcription, DNA-dependent; IEA.	AC	O40233;						
DR	InterPro; IPR004831; IV_Tat.	DT	01-JAN-1998	integrated into UniProtKB/TrEMBL.					
PFam; PF00339; Tat; 1.	DR	DT	01-JAN-1998	sequence version 1.					
PRINTS; PRO0055; HIVPATDOMAIN.	DR	DT	07-FEB-2006	entry version 25.					
Activator; Nuclear protein; RNA-binding; Transcription;	DR	DT		Tat protein (Fragment).					
Transcription regulation.	DR	DE		Name=tat;					
NON_TER 71	GN	OS	Human immunodeficiency virus 1.						
SEQUENCE 71 AA;	Qy	OC	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;						
8162 MW;	Db	OC	Lentivirus; Primate lentivirus group.						
SAFE3242E82321B3 CRC64;	Qy	OC	Medline+97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;						
55.0%; Score 11; DB 2; Length 71;	Db	OC	RA Kirchhoff F., Greenough T.C., Hamacher M., Sullivan J.L., NCBI_TaxID=11676;						
Best Local Similarity 100.0%; Pred. No. 0.00099;	Qy	RN	RN [1]						
Matches 11; Conservative 0; Mismatches 0;	Db	RN	NUCLEOTIDE SEQUENCE .						
Indels 0; Gaps 0;	Qy	RP	RT STRAIN=NR94-A3at;						
1 YGRKKRQRRL 11	Db	RX	RC MEDLINE+97335179; PubMed=9191845; DOI=10.1006/viro.1997.8586;						
47 YGRKKRQRRL 57	Qy	RA	RA Desrosiers R.C.;						
RT	Db	RA	"Activity of human immunodeficiency virus type 1 promoter/TAR regions and tat genes derived from individuals with different rates of disease progression.";						
RT	DR	RT	Virology 232:319-331(1997).						
RL	DR	RL	Virology 232:319-331(1997).						
CC	DR	CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms						
CC	DR	CC	Distributed under the Creative Commons Attribution-NoDerivs License						
CC	DR	CC	AF000531; AAB2530_1; - ; Genomic_DNA.						
CC	DR	DR	EMBL; PI2506; 1TBC.						
CC	DR	DR	HSSP; P04233; 1-71.						
CC	DR	DR	SMR; P04233; 1-71.						
CC	DR	DR	GO; GO:0042025; C:host cell nucleus; IEA.						
CC	DR	DR	GO; GO:0005634; C:nucleus; IEA.						
CC	DR	DR	GO; GO:0003723; F:RNA binding; IEA.						
CC	DR	DR	GO; GO:0003700; F:transcription factor activity; IEA.						
CC	DR	DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.						
CC	DR	DR	GO; GO:0006350; P:transcription; IEA.						
CC	DR	DR	GO; GO:0006350; P:transcription; IEA.						
CC	DR	DR	IntsPro; IPR01831; IV_Tat.						
CC	DR	DR	Pfam; PF00539; Tat; 1.						
CC	DR	DR	PRINTS; PRO0055; HIVPATDOMAIN.						
CC	DR	DR	Activator; Nuclear protein; RNA-binding; Transcription;						
CC	DR	DR	Transcription regulation.						
CC	DR	FT	FT NON_TER 71 AA; 8034 MW; SBBA79FB327EA3CD CRC64;						
CC	DR	FT	Query Match Score 11; DB 2; Length 71;						
CC	DR	FT	Best Local Similarity 100.0%; Pred. No. 0.00099;						
CC	DR	FT	Matches 11; Conservative 0; Mismatches 0;						
CC	DR	FT	Indels 0; Gaps 0;						
CC	DR	Qy	1 YGRKKRQRRL 11						
CC	DR	Db							
CC	DR	Db	47 YGRKKRQRRL 57						
CC	DR	DR	Search completed: August 24, 2006, 23:51:26						
CC	DR	DR	Job time : 301 secs						
CC	DR	FT	SEQUENCE 71 AA;						
CC	DR	FT	8226 MW;						
CC	DR	FT	324F908AF030E216 CRC64;						
CC	DR	FT	Query Match Score 11; DB 2; Length 71;						
CC	DR	FT	Best Local Similarity 100.0%; Pred. No. 0.00099;						
CC	DR	FT	Matches 11; Conservative 0; Mismatches 0;						
CC	DR	FT	Indels 0; Gaps 0;						

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OM protein - protein search, using sw model

Run on: August 24, 2006, 23:42:38 ; Search time 197 Seconds
(without alignments)

Title: US-10-814-109-2

Perfect score: 20

Sequence: 1 YGRKKRKRRRKPSADGHR 20

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2581586

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_8:
 1: GeneseqP1980s:
 2: GeneseqP1990s:
 3: GeneseqP2000s:
 4: GeneseqP2001s:
 5: GeneseqP2002s:
 6: GeneseqP2003s:
 7: GeneseqP2003bs:
 8: GeneseqP2004s:
 9: GeneseqP2005s:
 10: GeneseqP2006s:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	20	100.0	20	9	AED21152	Aed21152 SUDAPI-1/	
2	12	60.0	12	4	AAB83294	Aab83294 BBB Pepti	
3	12	60.0	12	4	AAB83295	Aab83295 BBB Pepti	
4	12	60.0	20	8	ADO20889	Ado20889 PSD-95 PD	
5	12	60.0	20	8	ADO20727	Ado20727 PSD-95 PD	
6	12	60.0	20	8	ADO20723	Ado20723 PSD-95 PD	
7	12	60.0	20	8	ADO20939	Ado20939 NMDA Rece	
8	12	60.0	20	8	ADO20674	Ado20674 PSD-95 PD	
9	12	60.0	20	8	ADO20637	Ado20637 PSD-95 PD	
10	12	60.0	20	8	ADO20730	Ado20730 PSD-95 PD	
11	12	60.0	20	8	ADU15784	Adu15784 MUC1-PDZ	
12	12	60.0	20	9	AEB07971	Aeb07971 Peptide b	
13	12	60.0	20	9	AEB07972	Aeb07972 Peptide b	
14	12	60.0	20	9	AEB07984	Aeb07984 Peptide 1	
15	11	55.0	11	2	AAW50263	Aaw50263 HIV-1 tat	
16	11	55.0	11	2	AYY50415	Ayy50415 TAT Pepti	
17	11	55.0	11	2	AYY25075	Aay25075 TAT trans	
18	11	55.0	11	3	AAB27088	Aab27088 Beta-acate	
19	11	55.0	11	3	AAB09807	Aab09807 HIV-tat p	
20	11	55.0	11	3	AYY93542	Ayy93542 Amino aci	
21	11	55.0	11	3	AYY71015	Aay71015 Human imm	
22	11	55.0	11	3	AAB35998	Aab35998 Peptide a	
23	11	55.0	11	3	AAB03961	Aab03961 Minimal e	

RESULT 1

AED21152
 ID AED21152 standard; peptide; 20 AA.
 XX
 AC AED21152;
 XX
 DT 01-DEC-2005 (first entry)
 XX
 DE SUDAPI-1/ HIV Tat domain fusion peptide, TSUDAPI-1 SEQ ID NO: 2.
 XX
 KW Protein interaction; therapeutic; cerebrovascular ischemia; multiple sclerosis;
 KW cerebroprotective; vasoactive; hypoxia; ischemia; neurotropic;
 KW neuroprotective; Huntington's chorea; anticonvulsant; neurotropic;
 KW parkinsons disease; antiparkinsonian; Alzheimer's disease; hyperglycemia;
 KW antidiabetic; diabetes; trauma; tranquilizer; pulmonary; epilepsy;
 KW grand mal seizure; muscle hypertension; muscle relaxant; paroxysms;
 KW muscular degenerat.; asthma; antiasthmatic; cardiac arrest; cardiotonic;
 KW macular degeneration; ophthalmological; psychiatric disorder;
 KW neuroleptic; schizophrenia; AIDS dementia complex; dementia;
 KW inflammation; antiinflammatory; pain; analgesic; opiate dependence;
 KW antaddictive; cocaine addiction; alcoholism; eating-disorders-gen.;
 KW anorexia nervosa; anabolic; eating-disorders-gen.;
 KW Src-unique domain anchoring protein inhibitor.

Location/Qualifiers
 1. .11 /note= "HIV transduction domain (TAT)"
 Region
 FT Region /note= "Src unique domain anchoring protein inhibitor 1"
 XX
 XX

12. .20 /note= "HIV transduction domain (TAT)"
 Region /note= "Src unique domain anchoring protein inhibitor 1"
 XX
 XX

US2005222042-A1.

XX

06-OCT-2005.

30-MAR-2004; 2004US-00814109.

30-MAR-2004; 2004US-00814109.

(HOSP-) HOSPITAL FOR SICK CHILDREN RES INST.
 Salter MW, Gingrich JR;

WPI; 2005-689427/1.

ALIGNMENTS

Modifying N-methyl-D-aspartate receptor interaction with non-receptor tyrosine kinase Src in cells, comprises administering composition comprising Src-unique domains anchoring protein inhibitor to cells.

Claim 13; SEQ ID NO 2; 32pp; English.

The present invention provides a method for modifying N-methyl-D-aspartate receptor (NMDA) interaction with non-receptor tyrosine kinase Src in cells. The method involves administering a composition including at least one Src-unique domain anchoring protein inhibitor (SUDAPI) to cells, where modification ameliorates a disease or condition related to NMDA signaling. Diseases or conditions ameliorated by the invention include stroke, hypoxia, ischemia, multiple sclerosis, Huntington's chorea, Parkinson's disease, Alzheimer's disease, hyperglycemia, diabetes, traumatic injury, epilepsy, grand mal seizures, spasticity, cerebral palsy, asthma, cardiac arrest, macular degeneration, mental diseases, schizophrenia, AIDS dementia complex, other dementias, AIDS wasting syndrome, inflammation, pain, opioid addiction, cocaine addiction, alcohol addiction and other conditions associated with substance abuse and anorexia. The present sequence is the SUDAPI-I/HIV Tat domain fusion peptide, TSUDAPI-I.

peptide sequence is a BBB peptide which may be a peptide. Pulmonary drug delivery is useful as therapeutic agent may be a peptide. Pulmonary drug delivery is useful as it increases the drug retention time in the lungs and reduces the risk of extrapharmacological side effects. Modified therapeutic agents of this type may be antihistamines, anti-angina, anti-hypertensive or anti-arrhythmic agents, anti-depressants, bronchodilators, opioids or their analogues, anti-inflammatory agents, or anti-thyroid deficiency agents. The present

```

2 Sequence 20 AA;
2 Query Match :.....;
2 Score 20.00; DB 9; Length 20;
2
```

RESULT 2

RESULT 2
AB83294
AAB8

X Synthetic.
X WO200117568-A2.
X 15-MAR-2001.
X 07-SEP-2000; 2000WO-TB001429.
X 07-SEP-1999; 99US-0152661P.
X (CONJ-) CONJUCHEM INC.
X Ezrin AM, Flesser A, Robitaille M, Milner PG, Bridon DP,
X WPI; 2001-354657/37.
X Pulmonary delivery of therapeutic agents which are capable of forming
PT covalent bonds with amino, hydroxyl or thiol groups on pulmonary or blood
PT components.
XX Example 15; Page 141; 104pp; English.
PS DR WPI; 2001-354657/37.
XX Pulmonary delivery of therapeutic agents which are capable of forming
PT covalent bonds with amino, hydroxyl or thiol groups on pulmonary or blood
PT components.
XX The present invention describes a modified therapeutic agent comprising
CC therapeutic agent and a reactive group which reacts with groups on
CC pulmonary or blood components to form a stable covalent bond, where the
CC therapeutic agent may be a peptide. Pulmonary drug delivery is useful as
CC it increases the drug retention-time in the lungs and reduces the risk of
CC extrapulmonary side effects. Modified therapeutic agents of this type may
CC be antihistamines, anti-angina, anti-hypertensive or anti-arrhythmic
CC agents, anti-depressants, bronchodilators, opioids or their analogues,
CC anti-inflammatory agents, or anti-thyroid deficiency agents. The present
CC sequence is a BBR peptide.

Sequence 12
 XX
 SQ Sequence 12 AA;
 Query Match 60.0%; Score 12; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 12; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;


```

Query Match          60.0%; Score 12; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0
1 YGKKKKRRRKK 12
1 YGKKKKRRRKK 12

```

RESULT 7
D020599 standard; peptide; 20 μ A.
D ADD020599
X
C ADD020599;
X
T 26-AUG-2004 (first entry)
X NMDA receptor PSD-95 binding inhibitor peptide #4.
X neuroprotective; gene therapy; N-methyl D-aspartate receptor;
X NMDA receptor; PDZ domain; PDZ protein; binding inhibitor;

DB	PSD-95 PDZ domain binding peptide #16.
KW	neuroprotective; gene therapy; N-methyl-D-aspartate receptor; NMDA receptor; PDZ domain; PDZ protein; binding inhibitor; neuronal disorder; stroke; ischaemia; PSD-95; PDZ domain.
KW	Unidentified.
XX	OS
XX	XX

PN	WO2004045535-A2.
XX	XX
PD	03 -JUN-2004 .
XX	XX
PF	14 -NOV -2003 ; 2003WO-US036698 .
XX	XX
PR	14 -NOV -2002 ; 2002US-042212P .
PR	14 -NOV -2002 ; 2002US-0426213P .
XX	XX
PA	(ARBO-) ARBOR VITA CORP .
XX	XX
PI	Lu PS, Garman JD, Belmares MP;
XX	XX
DR	WPI; 2004-420526/39 .
XX	XX
PT	New pharmaceutical composition comprising a polypeptide that inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PSD protein.

The invention describes a pharmaceutical composition comprising an isolated, recombinant or synthetic polypeptide that inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein and a carrier, diluent or excipient and that comprises a C-terminal amino acid sequence of X-Thr-X-Val-Leu-Ala. Also described are: an isolated, recombinant or synthetic polypeptide for use in therapy and that comprises a C-terminal amino acid sequence of X-Thr-X-Val-Leu-Ala and inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein; and a method for determining whether a test compound inhibits binding between a PDZ protein and a N-methyl-D-aspartate (NMDA) receptor. The pharmaceutical composition is useful in treating a neuronal disorder, which is an injury caused by stroke or ischaemia. This is the amino acid sequence of a PDZ domain ligand that binds to the PDZ domain of PSD-95.

Query Match 60.0%; Score 12; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.00022;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1	YGRKRRQRKK	12
1	YGRKRRQRKK	12

SU LT 9
AD020697 standard; peptide; 20 AA.

AD020697;

26-AUG-2004 (First entry)

PSD-95 PDZ domain binding peptide #39.

neuroprotective; gene therapy; N-methyl-D-aspartate receptor; NMDA receptor; PDZ domain; PDZ protein; binding inhibitor; neuronal disorder; stroke; ischaemia; PSD-95; PDZ domain. Unidentified.

WO2004045535-A2.

03-JUN-2004.

14-NOV-2003; 2003WO-US036698.

14-NOV-2002; 2002US-0426212P.
14-NOV-2002; 2002US-0426213P.

(ARBO-) ARBOR VITA CORP.

Lu PS, Garman JD, Beimares MP;

WPI; 2004-420526/39.

New pharmaceutical composition comprising a polypeptide that inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein, useful in treating a neuronal disorder e.g. an injury caused by stroke or ischemia.

Example 9; Page 105; 146pp; English.

The invention describes a pharmaceutical composition comprising an isolated, recombinant or synthetic polypeptide that inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein and a carrier, diluent or excipient and that comprises a C-terminal amino acid sequence of X-Thr-X-Val/IleuAla. Also described are: an isolated,

CC	recombinant or synthetic polypeptide for use in therapy and that
CC	comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala and
CC	inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ
CC	protein; and a method for determining whether a test compound inhibits
CC	binding between a PDZ protein and a N-methyl-D-aspartate (NMDA) receptor.
CC	The pharmaceutical composition is useful in treating a neuronal disorder,
CC	which is an injury caused by stroke or ischaemia. This is the amino acid
CC	sequence of a PDZ domain ligand that binds to the PDZ domain of PSD-95.
XX	Sequence 20 AA;
SO	Query Match 60.0%; Score 12; DB 8; Length 20;
SO	Best Local Similarity 100.0%; Pred. No. 0.00022;
SO	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 YGRKKRQRRK 12 1 YGRKKRQRRK 12
Db	
RESULT 10	
ADO20730	ADO20730 standard; peptide; 20 AA.
XX	XX
XX	AC ADO20730;
XX	DT 26-AUG-2004 (first entry)
XX	DE PSD-95 PDZ domain binding peptide #72.
XX	KW neuroprotective; gene therapy; N-methyl-D-aspartate receptor;
XX	KW NMDA receptor; PDZ domain; binding inhibitor;
XX	KW neuronal disorder; stroke; ischaemia; PSD-95; PDZ domain.
XX	Unidentified.
OS	XX
XX	WO2004045535-A2.
PN	XX
XX	03-JUN-2004.
PD	XX
PF	14-NOV-2003; 2003WO-US016698.
XX	XX
PR	14-NOV-2002; 2002US-042612P.
PR	14-NOV-2002; 2002US-042613P.
XX	XX
PA	(ARBO-) ARBOR VITA CORP.
XX	XX
PI	Lu PS, Garman JD, Belmonte MP;
XX	XX
DR	WPI; 2004-420526/39.
XX	XX
PT	New pharmaceutical composition comprising a polypeptide that inhibits
PT	binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein,
PT	useful in treating a neuronal disorder e.g. an injury caused by stroke or
PT	ischemia.
XX	XX
PS	Example 9; Page 105; 146pp; English.
XX	XX
CC	The invention describes a pharmaceutical composition comprising an
CC	isolated, recombinant or synthetic polypeptide that inhibits binding
CC	between a N-methyl-D-aspartate (NMDA) receptor and a PDZ protein and a
CC	carrier, diluent or excipient and that comprises a C-terminal amino acid
CC	sequence of X-Thr-X-Val/Leu/Ala. Also described are: an isolated,
CC	recombinant or synthetic polypeptide for use in therapy and that
CC	comprises a C-terminal amino acid sequence of X-Thr-X-Val/Leu/Ala and
CC	inhibits binding between a N-methyl-D-aspartate (NMDA) receptor and a PDZ
CC	protein; and a method for determining whether a test compound inhibits
CC	binding between a PDZ protein and a N-methyl-D-aspartate (NMDA) receptor.
CC	The pharmaceutical composition is useful in treating a neuronal disorder,
CC	which is an injury caused by stroke or ischaemia. This is the amino acid
CC	sequence of a PDZ domain ligand that binds to the PDZ domain of PSD-95.
XX	Sequence 20 AA;
SO	

channel proteins or cellular protein interaction domains that effect the CC TRP channel protein interactions) and determining whether a test compound CC modulates binding between a TRP channel protein and a PDZ domain- CC containing polypeptide (comprising contacting a TRP channel protein and a PDZ domain- CC sequence with a PDZ domain-containing polypeptide, and measuring the amount of complex formed between the TRP channel PDZ-Ligand sequence and the PDZ domain-containing polypeptide). The TRP-associated protein in the CC inhibitor cited above comprises at least one PDZ domain selected from RIM -2, Mint 1, INADL, Syntriphin 1 alpha, SITAC-18, LIM mystique, 20-1, PAR3L, MAST2, PARS, and novel serine protease. The TRP channel protein is human TRPM7 or mouse TRPM7. The methods and compositions of the present invention are useful for reducing the damaging effect of an injury to mammalian cells, including brain and spinal cord cells, by treatment with compounds which reduce cell death or dysfunction, including cellular damage following episodes of tissue ischemia and trauma. Also treatable with the methods and compositions and acute or chronic degeneration, such as in stroke, epilepsy, Parkinson's disease, glaucoma, Alzheimer's disease, spinal cord injuries, myocardial ischemia, Huntington's chorea, inherited ataxias and motor neuron disease. The present sequence is a peptide tested for its ability to bind to a selected PDZ domain or inhibit the binding of the PDZ domain to a TRP protein.

XX Sequence 20 AA;

Query Match 60.0%; Score 12; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRKQRQQRK 12
 ||||| | | | | | |
Db 1 YGRKKRKQRQQRK 12

RESULT 13

AEB07972

ID AEB07972 standard; peptide; 20 AA.

AC AEB07972;

DT 08-SEP-2005 (first entry)

DE Peptide binding to RIM2 PDZ domain 1 SEQ ID 364.

KW Protein interaction; protein therapy; TRP; cell death; PDZ domain; KW transient receptor potential channel; TRP; cell death; PDZ domain; KW Vasotocine; Nootropic; Neuroprotective; Ophthalmological; KW Antiparkinsonian; Anticonvulsant; cerebroprotective; pulmonary; cardiant; muscular-gen.; CNS-gen.; brain injury; spinal cord injury; ischemia; trauma; degeneration; cerebrovascular ischemia; epilepsy; Parkinson's disease; glaucoma; Alzheimer's disease; myocardial ischemia; Huntington's chorea; ataxia; motor neuron disease.

XX OS Synthetic.

PN WO2005061548-A1.

XX PD 07-JUL-2005.

XX XX 22-DEC-2004; 2004WO-CA002193.

XX PR 23-DEC-2003; 2003US-0532169P.

XX PA (ARBO-) ARBOR VITA CORP.

PA (NONO-) NONO INC.

PI Tyminski M, Garman JD, Belmares MP;

XX DR 2005-479449/48.

XX New isolated polypeptides inhibiting binding between a transient receptor potential (TRP) channel protein and a TRP-associated protein, useful in reducing damage to mammalian cells following stroke, epilepsy or spinal cord injuries.

XX

PS Example 3; SEQ ID NO 364; 377bp; English.

XX The invention relates to an inhibitor comprising an isolated, recombinant CC or synthetic polypeptide that inhibits binding between a transient receptor potential (TRP) channel protein and a TRP-associated protein (e.g., one containing a PDZ domain). Also included are a pharmaceutical composition comprising the inhibitor cited above (and a physiological carrier, diluent or excipient), an inhibitor comprising a nucleic acid sequence capable of inhibiting the expression of a TRP channel protein post transcriptionally, treating mammalian cell injury (comprising and a introducing a modulator of binding between a TRP channel protein and a TRP channel associated protein into a cell), reducing the damaging effect of ischemia/tramatic injury to the brain/spinal cord in a mammal (comprising treating the mammal with a non-toxic, damage-reducing, effective amount of a modulator of binding between a TRP channel protein and a TRP channel associated protein), controlling the concentration of Ca²⁺-dependent signaling molecules in the vicinity of ion channel pores of cells in vivo (to prevent the diffusion of toxic amounts of the Ca²⁺, influx) to prevent the triggering of neurotoxic phenomena (comprising administering an effective, non-toxic amount of a modulator of TRP channel proteins or cellular protein interaction domains that effect the TRP channel protein interactions) and determining whether a test compound CC modulates binding between a TRP channel protein and a PDZ domain-containing polypeptide (comprising contacting a TRP channel PDZ-ligand sequence with a PDZ domain-containing polypeptide), and measuring the amount of complex formed between the TRP channel PDZ-ligand sequence and the PDZ domain-containing polypeptide). The TRP-associated protein in the inhibitor cited above comprises at least one PDZ domain selected from RIM -2, Mint 1, INADL, Syntrphin 1 alpha, SITAC-18, LIM mystique, 20-1, PAR3L, MAST2, PARS, and novel serine protease. The TRP channel protein is human TRPM7 or mouse TRPM7. The methods and compositions of the present invention are useful for reducing the damaging effect of an injury to mammalian cells, including brain and spinal cord cells, by treatment with compounds which reduce cell death or dysfunction, including cellular damage following episodes of tissue ischemia and trauma. Also treatable with the methods and compositions and acute or chronic degeneration, such as in stroke, epilepsy, Parkinson's disease, glaucoma, Alzheimer's disease, spinal cord injuries, myocardial ischemia, Huntington's chorea, ataxia; peptide tested for its ability to bind to a selected PDZ domain or inhibit the binding of the PDZ domain to a TRP protein.

XX SQ Sequence 20 AA;

Query Match 60.0%; Score 12; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGRKKRKQRQQRK 12
 ||||| | | | | | |
Db 1 YGRKKRKQRQQRK 12

RESULT 14

AEB07884

ID AEB07884 standard; peptide; 20 AA.

XX AC AEB07884;

DT 08-SEP-2005 (first entry)

XX XX Peptide inhibitor of TRPM7-ZO-1/INADL PDZ domains, 1852.

XX KW Protein interaction; protein therapy; transient receptor potential channel; TRP; cell death; PDZ domain;

KW Vasotocine; Nootropic; Neuroprotective; Ophthalmological;

KW Antiparkinsonian; Anticonvulsant; cerebroprotective; pulmonary; cardiant;

KW muscular-gen.; CNS-gen.; brain injury; spinal cord injury; ischemia;

KW trauma; degeneration; cerebrovascular ischemia; epilepsy;

KW Parkinson's disease; glaucoma; Alzheimer's disease; myocardial ischemia;

KW Huntington's chorea; ataxia; motor neuron disease.

XX OS Synthetic.

PN WO2005061548-A1.

XX PD 07-JUL-2005.

XX XX 22-DEC-2004; 2004WO-CA002193.

XX PR 23-DEC-2003; 2003US-0532169P.

XX PA (ARBO-) ARBOR VITA CORP.

PA (NONO-) NONO INC.

PI Tyminski M, Garman JD, Belmares MP;

XX DR 2005-479449/48.

XX New isolated polypeptides inhibiting binding between a transient receptor potential (TRP) channel protein and a TRP-associated protein, useful in reducing damage to mammalian cells following stroke, epilepsy or spinal

PT cord injuries.

OS Synthetic.
 XX WO2005061548-A1.
 PN XX RESULT 15
 PD XX AAW50263 standard; protein; 11 AA.
 XX ID AAW50263
 XX XX
 XX AC AAW50263;
 XX DT 17-OCT-2003 (revised)
 PR XX DT 20-JUL-1998 (first entry)
 XX HIV-1 tat protein.
 XX DE HIV-1 tat protein.
 XX KW Mouse; BH3 interacting domain death agonist; BID; BCL-2 family;
 PR KW apoptosis; regulation; cell death; inflammation; cancer; arthritis;
 PA KW autoimmune disease; viral infection; lymphoproliferative.
 XX HIV/AIDS; hepatitis C virus; hepatitis B virus; hepatitis C; hepatitis B;
 PI HIV-1; HIV-2; hepatitis C virus; hepatitis B virus; hepatitis C; hepatitis B;
 XX HIV/AIDS; hepatitis C virus; hepatitis B virus; hepatitis C; hepatitis B;
 DR WPI; 2005-479449/48.
 XX New isolated polypeptides inhibiting binding between a transient receptor
 PR potential (TRP) channel protein and a TRP-associated protein, useful in
 PR reducing damage to mammalian cells following stroke, epilepsy or spinal
 PR cord injuries.
 PR Example 3; SEQ ID NO 276; 377pp; English.
 PS XX The invention relates to an inhibitor comprising an isolated, recombinant
 CC or synthetic polypeptide that inhibits binding between a transient
 CC receptor potential (TRP) channel protein and a TRP-associated protein
 CC (e.g. one containing a PDZ domain). Also included are a pharmaceutical
 CC composition comprising the inhibitor cited above (and a physiologically
 CC carrier, diluent or excipient), an inhibitor comprising nucleic acid
 CC sequence capable of inhibiting the expression of a TRP channel protein
 CC post transcriptionally, treating mammalian cell injury (comprising
 CC introducing a modulator of binding between a TRP channel protein and a
 CC TRP channel associated protein in a cell), reducing the damaging effect
 CC of ischaemia/trumatic injury to the brain/spinal cord in a mammal
 CC comprising treating the mammal with non-toxic, damage-reducing,
 CC effective amount of a modulator of binding between a TRP channel protein
 CC and a TRP channel associated protein, controlling the concentration of
 CC Ca²⁺-dependent signalling molecules in the vicinity of ion channel pores
 CC of cells in vivo (to prevent the diffusion of toxic amounts of the
 CC Ca²⁺ influx, to prevent the triggering of neurotoxic phenomena (comprising
 CC administering an effective non-toxic amount of a modulator of TRP
 CC channel proteins or cellular protein interaction domains that effect the
 CC TRP channel protein interactions) and determining whether a test compound
 CC modulates binding between a TRP channel protein and a PDZ domain
 CC containing polypeptide (comprising contacting a TRP channel PDZ-Ligand
 CC sequence with a PDZ domain-containing polypeptide, and measuring the
 CC amount of complex formed between the TRP channel PDZ-Ligand sequence and
 CC the PDZ domain-containing polypeptide). The TRP-associated protein in the
 CC inhibitor cited above comprises at least one PDZ domain selected from RIM
 CC -2, Mint 1, INAD, Syntrphin 1 alpha, STAC-1B, LIM myctine, ZO-1,
 CC PAR3L, MAST2, PARS, and novel serine procase. The TRP channel protein is
 CC a human TRPM7 or mouse TRPM7. The methods and compositions of the present
 CC invention are useful for reducing the damaging effect of an injury to
 CC mammalian cells, including brain and spinal cord cells, by treatment with
 CC compounds which reduce cell death or dysfunction, including cellular
 CC damage following episodes of tissue ischemia and trauma. Also treatable
 CC with the methods and compositions and acute or chronic degeneration, such
 CC as in stroke, epilepsy, Parkinson's disease, glaucoma, Alzheimer's
 CC disease, spinal cord injuries, myocardial ischemia, Huntington's chorea,
 CC inherited ataxias and motor neurone disease. The present sequence is a
 CC peptide tested for its ability to bind to a selected PDZ domain or
 CC inhibit the binding of the PDZ domain to a TRP protein.
 XX Sequence 20 AA:
 SQ Query Match 55.0%; Score 11; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 YGRKQRQRRR 11
 Db 1 YGRKQRQRRR 11

Search completed: August 24, 2006, 23:46:23
 Job time : 200 secs

Scoring table:	BLOSUM62					
Gapped:	Gapext 0.5					
Searched:	2849598 seqs, 925015592 residues					
Total number of hits satisfying chosen parameters:	2849598					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries					
Database :	UniProt 7.2: 1: uniprot_sprot: 2: uniprot_trembl: *					
Pred. No.	The number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES						
Result No.	Query	Match	Length	DB	ID	Description
1	81	75.7	101	2	Q3SSPF8_9HIV1	Q3SSPF8 human immun
2	80	74.8	101	2	Q5EFXK8_9HIV1	Q5EFXK8 human immun
3	80	74.8	101	2	Q6BBP4_9HIV1	Q6BBP4 human immun
4	80	74.8	101	2	Q8U5Z0_9HIV1	Q8U5Z0 human immun
5	79	73.8	101	2	Q3SSP9_9HIV1	Q3SSP9 human immun
6	79	73.8	101	2	Q6X6S0_9HIV1	Q6X6S0 human immun
7	79	73.8	101	2	Q8QDF8_9HIV1	Q8QDF8 human immun
8	79	73.8	101	2	Q9001L_9HIV1	Q9001L human immun
9	78	72.9	71	2	Q5UGB1_9HIV1	Q5UGB1 human immun
10	78	72.9	71	2	Q5UGB1_9HIV1	Q5UGB1 human immun
11	78	72.9	71	2	Q8ATV7_9HIV1	Q8ATV7 human immun
12	78	72.9	72	2	Q8UNM5_9HIV1	Q8UNM5 human immun
13	78	72.9	72	2	Q8UNM6_9HIV1	Q8UNM6 human immun
14	78	72.9	72	2	Q8UNM7_9HIV1	Q8UNM7 human immun
15	78	72.9	72	2	Q8UNM8_9HIV1	Q8UNM8 human immun
16	78	72.9	72	2	Q8UNN1_9HIV1	Q8UNN1 human immun
17	78	72.9	72	2	Q8UNN4_9HIV1	Q8UNN4 human immun
18	78	72.9	72	2	Q8UNN6_9HIV1	Q8UNN6 human immun
19	78	72.9	72	2	Q8UNN9_9HIV1	Q8UNN9 human immun
20	78	72.9	72	2	Q8UNM0_9HIV1	Q8UNM0 human immun
21	78	72.9	72	2	Q8UNM2_9HIV1	Q8UNM2 human immun
22	78	72.9	99	2	Q8UT76_9HIV1	Q8UT76 human immun
23	78	72.9	101	2	Q90085_9HIV1	Q90085 human immun
24	78	72.9	101	2	Q4USB2_9HIV1	Q4USB2 human immun
25	78	72.9	101	2	Q5FXR6_9HIV1	Q5FXR6 human immun
26	78	72.9	101	2	Q5FXU2_9HIV1	Q5FXU2 human immun
27	78	72.9	101	2	Q6S802_9HIV1	Q6S802 human immun
28	78	72.9	101	2	Q6XGJ5_9HIV1	Q6XGJ5 human immun
29	78	72.9	101	2	Q6XGU8_9HIV1	Q6XGU8 human immun
30	78	72.9	101	2	Q9OCH6_9HIV1	Q9OCH6 human immun
31	78	72.9	101	2	Q9OCY2_9HIV1	Q9OCY2 human immun

RESULT 5				
ID Q55P9_9HIV1	PRELIMINARY;	PRT;	101 AA.	
ID OT55P9_				
AC Q55P9_				
DR 11-OCT-2005, integrated into UniProtKB/TremBL.				
DR 11-OCT-2005, sequence version 1.				
DR 07-FEB-2006, entry version 4.				
Tat protein.				
GN Name=tat;				
OS Human immunodeficiency virus 1.				
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;				
OC Lentivirus; Primate lentivirus group.				
OX NCBI_TaxID=11676;				
RN [1]				
RP NUCLEOTIDE SEQUENCE.				
RC STRAIN=042AS16IB1;				
RA Birditt B.A., Rousseau C.M., Korber B.T., Goulder P., Brander C.,				
RA Kiepiela P., Walker B.D., Mullins J.I.;				
RT "HIV HLA epitope mapping from Durban, South Africa.";				
RL Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.				
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CC				
DR EMBL; DOI:164115; AAZ91841.1; Genomic RNA.				
DR GO; GO:004205; C:host cell nucleus; IEA.				
DR GO; GO:0005634; C:nucleus; IEA.				
DR GO; GO:003223; P:RNA binding; IEA.				
DR GO; GO:003700; F:transcription factor activity; IEA.				
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.				
DR GO; GO:0006350; P:transcription; IEA.				
DR InterPro; IPR01831; IV_Rat.				
DR Pfam; PF00539; Tat; 1.				
DR PRINTS; PR00055; HIVATDOMAIN.				
KW Activator; Nuclear protein; RNA-binding; Transcription;				
KW Transcription regulation.				
SQ SEQUENCE 101 AA; 11459 MW; 79E2BB916116356F CRC64;				
Query Match 73.8%; Score 79; DB 2; Length 101;				
Best Local Similarity 70.0%; Pred. No. 0.00089; Mismatches 3; Indels 0; Gaps 0;				
Matches 14; Conservative 3; MisMatches 3; Indels 0; Gaps 0;				
CC				
Qy 1 YGRKKRQRRRKPSADGHR 20				
Db 47 YGRKKRQRRSPSSSEGHQ 66				
RESULT 7				
Q8ODF8_9HIV1	PRELIMINARY;	PRT;	101 AA.	
ID Q8ODF8_9HIV1				
AC Q8ODF8;				
DR 01-JUN-2002, integrated into UniProtKB/TremBL.				
DR 01-JUN-2002, sequence version 1.				
DR 07-FEB-2006, entry version 16.				
DE Tat protein.				
GN Name=tat;				
OS Human immunodeficiency virus 1.				
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;				
OC Lentivirus; Primate lentivirus group.				
OX NCBI_TaxID=11676;				
RN RN NUCLEOTIDE SEQUENCE.				
RA Novitsky V.;				
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.				
CC CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms				
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CC CC DR EMBL; AY074891; AAL7049.1; -; Genomic_DNA.				
DR HSSP; P04610; IUEW.				
DR SMR; QBQDF8; 1-86.				
DR GO; GO:0042025; C:host cell nucleus; IEA.				
DR GO; GO:0005634; C:nucleus; IEA.				
DR GO; GO:003223; P:RNA binding; IEA.				
DR GO; GO:0003700; F:transcription factor activity; IEA.				
DR InterPro; IPR01831; IV_Rat.				
DR Pfam; PF00539; Tat; 1.				
DR PRINTS; PR00055; HIVATDOMAIN.				
KW Activator; Nuclear protein; RNA-binding; Transcription;				
KW Transcription regulation.				
SQ SEQUENCE 101 AA; 11504 MW; 80EACA7E87C349A CRC64;				
Query Match 73.8%; Score 79; DB 2; Length 101;				
Best Local Similarity 70.0%; Pred. No. 0.00089; Mismatches 3; Indels 0; Gaps 0;				
Matches 14; Conservative 3; MisMatches 3; Indels 0; Gaps 0;				
CC				
Qy 1 YGRKKRQRRRKPSADGHR 20				
Db 47 YGRKKRQRRSPSSSEGHQ 66				
RESULT 6				
Q6X6H0_9HIV1	PRELIMINARY;	PRT;	101 AA.	
ID Q6X6H0_				
AC Q6X6H0;				
DR 05-JUL-2004, integrated into UniProtKB/TremBL.				
DR 05-JUL-2004, sequence version 1.				
DR 07-FEB-2006, entry version 10.				
DE Tat protein.				
GN Name=tat;				
OS Human immunodeficiency virus 1.				
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;				
OC Lentivirus; Primate lentivirus group.				
OX NCBI_TaxID=11676;				
RN RNCLEOTIDE SEQUENCE.				
RP PubMed=15320594; DOI=10.1089/088932204172535;				
RA Arroyo M.A., Hoelscher M., Sanders-Buell E., Herbigger K.H., Samky E.,				
RA Maboko L., Hoffmann O., Robb M.R., Brix D.L., McCutchan F.E.;				
RT "HIV Type 1 Subtypes among Blood Donors in the Mbeya Region of				
RT Southwest Tanzania"; AIDS Res. Hum. Retroviruses 20:895-901 (2004).				
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DR EM253322; ARQ98283.1; -; Genomic_DNA.				
RESULT 8				
Q900L1_9HIV1	PRELIMINARY;	PRT;	101 AA.	
ID Q900L1_9HIV1				
AC Q900L1_				

DT 01-DEC-2001, integrated into UniProtKB/TremBL.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 17.
 DE Name=taxt;
 GN Virus; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Lentivirus; Primate lentivirus group.
 OC NCBI_TaxID=11676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE;
 MEDLINE=21828182; PubMed=11039148; DOI=10.1089/08892220252779692;
 RA Scriba T.J., de Villiers T., Treurnicht F.K., zur Negede J.,
 RA Barnett S.W., Engelbrecht S., van Rensburg E.J.;
 RT "Characterization of the South African HIV type 1 subtype C complete
 RT 5' long terminal repeat, nef, and regulatory genes.",
 RL AIDS Res. Hum. Retroviruses 18:149-159(2002).
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 CC
 DR EMBL; AY047269; AL06105.1; -; Genomic DNA.
 DR EMBL; AY047268; AL06105.1; JOINED; Genomic_DNA.
 DR HSSP; P0433; 1KSK.
 DR GO; GO:0042025; C: host cell nucleus; IEA.
 DR GO; GO:0005634; C: nucleolus; IEA.
 DR GO; GO:0003223; RNA binding; IEA.
 DR GO; GO:0003700; Filtranscription factor activity; IEA.
 DR GO; GO:0006355; Filtranscription of transcription, DNA-dependent; IEA.
 DR GO; GO:0006350; Filtranscription; IEA.
 DR InterPro; IPR01833; IV_rat.
 DR Pfam; PF00539; Tat_1.
 DR PRNTS; PR00055; HIV1TDOMAIN.
 DR Activator; Nuclear protein; RNA-binding; Transcription;
 DR Transcription regulation; IEA.
 SQ SEQUENCE 101 AA; 601D4736B6816EFO CRC64;
 DR
 Query Match Score 73.8%; DB 2%; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0089; Length 101;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 DR
 Qy 1 YGRKKRKRRKPKASADGHR 20
 db 47 YGRKKRKRRKPKASSEGHQ 66
 DR
 RESULT 9
 Q5UGBO_9HIV1 PRELIMINARY; PRT; 71 AA.
 ID Q5UGBO_9HIV1 PRELIMINARY; PRT; 71 AA.
 AC Q5UGBO;
 DT 07-DEC-2004, integrated into UniProtKB/TremBL.
 DT 07-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Tat protein (Fragment).
 DE Name=taxt;
 OS Human immunodeficiency virus 1.
 OS Viruses: Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Lentivirus; Primate lentivirus group.
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 STRAIN=B049BB;
 RC Herring B.L., Grant R.M., Delwart E.L.;
 NCBI_TaxID=11676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Herring B.L., Grant R.M., Delwart E.L.;
 OC Lentivirus; Primate lentivirus group.
 OC NCBITaxID=11676;
 RN [1]
 RP Activator; Nuclear protein; RNA-binding; Transcription;
 KW Transcription regulation.
 FT NON_TER 71 71 MW; 20E0B9AF0C69EAF6 CRC64;
 SQ SEQUENCE 71 AA; 8235 MW;
 DR
 Query Match Score 72.9%; DB 2%; Length 71;
 Best Local Similarity 70.0%; Pred. No. 0.0087; Length 71;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 DR
 Qy 1 YGRKKRKRRKPKASADGHR 20
 db 47 YGRKKRKRRKPKASSEGHQ 66
 DR
 RESULT 11
 Q5ATV7_9HIV1

Q8ATV7_9HIV1 PRELIMINARY; PRT; 71 AA.
 Q8ATV7_9HIV1 PRELIMINARY; PRT; 71 AA.
 AC GO; GO:0003700; F:transcription factor activity; IEA.
 AC GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DT 01-MAR-2003, integrated into UniProtKB/TREMBL.
 DT 01-MAR-2003, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DT Tat protein (Fragment).
 Name=tat;
 Human immunodeficiency virus 1.
 Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 Lentivirus; Primate lentivirus group.
 NCBI_TaxID=11676; [1]
 RN NUCLEOTIDE SEQUENCE.
 RP Nanteca M.B., Yirrell D.L., Kintu P., Kaleebu P., Biryahwaho B.,
 RA Morgan D., Whitworth J.; submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; AF425969; ANN31625.1; -; Genomic_DNA.
 DR HSSP; P04613; 1K5K.
 DR SMR; Q8ATV7; 1-71.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:transcription factor regulation; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR01831; IV_Tat.
 DR Pfam; PF00539; Tat; 1.
 DR PRINTS; PRO0055; HIVTATDOMAIN.
 DR Activator; Nuclear protein; RNA-binding; Transcription;
 DR Transcription regulation.
 DR NON_TER 71 71
 SQ SEQUENCE 71 AA; 8243 MW; 3D10B9A460729AF2 CRC64;

 Query Match Score 78; DB 2; Length 71;
 Best Local Similarity 70.0%; Pred. No. 0.00087;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

 Qy 1 YGRKKRKQRKRKPKASADGHR 20
 DR 47 YGRKKRKQRKRSPQQSAHQ 66

 RESULT 13 Q8UMMS_9HIV1 PRELIMINARY; PRT; 72 AA.
 ID Q8UMMS_9HIV1 PRELIMINARY; PRT; 72 AA.
 AC GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 AC GO; GO:0005634; C:nucleus; IEA.
 DT 01-MAR-2002, integrated into UniProtKB/TREMBL.
 DT 01-MAR-2002, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DT Tat protein (Fragment).
 Name=tat;
 Human immunodeficiency virus 1.
 Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 Lentivirus; Primate lentivirus group.
 NCBI_TaxID=11676; [1]
 RN NUCLEOTIDE SEQUENCE.
 RP Ranga U., Nagendran R., Siddappa N.B., Mahadevan A., Parthasarathy S.,
 RA Shankar S.K.; submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL; AY054236; AAU51174.1; -; Genomic_DNA.
 DR HSSP; P12506; 1TBC.
 DR Ranga U., Nagendran R., Siddappa N.B., Mahadevan A., Parthasarathy S.,
 RA Shankar S.K.; submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RL DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR01831; IV_Tat.
 DR Pfam; PF00539; Tat; 1.
 DR PRINTS; PRO0055; HIVTATDOMAIN.
 DR Activator; Nuclear protein; RNA-binding; Transcription;
 DR Transcription regulation.
 DR NON_TER 72 72
 SQ SEQUENCE 72 AA; 8385 MW; 656790CF4999FE3B CRC64;

 Query Match Score 78; DB 2; Length 72;
 Best Local Similarity 70.0%; Pred. No. 0.00086;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

 Qy 1 YGRKKRKQRKRKPKASADGHR 20
 DR 47 YGRKKRKQRKRSPQQSAHQ 66

 RESULT 14 Q8UMM7_9HIV1 PRELIMINARY; PRT; 72 AA.
 ID Q8UMM7_9HIV1 PRELIMINARY; PRT; 72 AA.
 AC GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 AC GO; GO:0005634; C:nucleus; IEA.
 DT 01-MAR-2002, integrated into UniProtKB/TREMBL.
 DT 01-MAR-2002, sequence version 1.
 DR EMBL; AY064237; AAU51175.1; -; Genomic_DNA.
 DR HSSP; P12506; 1TBC.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0005633; C:nucleus; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.

DT 07-FEB-2006, entry version 16.
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
NCBI_TaxID=11676;
RN [1] _NUCLEOTIDE_SEQUENCE; RA Ranga U., Nagendran R., Siddappa N.B., Mahadevan A., Parthasarathy S.,
RA Shankar S.K.; Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AY064235; AL51173_1; -; Genomic_DNA.
DR HSSP; P12506; ITBC.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:005634; C:nucleus; IEA.
DR GO; GO:000722; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0001550; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat_1.
DR PRINTS; PR00055; HIVTDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription;
KW Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA; 8428 MW; 13BCE610D7E0062B CRC64;
Query Match 72.9%; Score 78; DB 2; Length 72;
Best Local Similarity 70.0%; Pred. No. 0.00088;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db 47 YGRKERRQRRKPASADGHR 20
Db 47 YGRKERRQRRKPASSEDHQ 66

RESULT 15
QBUNM8 9HIV1 ID QBUMM8_9HIV1 PRELIMINARY; PRT; 72 AA.
AC QBUMM8;
DT 01-MAR-2002, integrated into UniProtKB/tREMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-FEB-2006, entry version 16.
DB Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
NCBI_TaxID=11676;
RN [1] _NUCLEOTIDE_SEQUENCE; RA Ranga U., Nagendran R., Siddappa N.B., Mahadevan A., Parthasarathy S.,
RA Shankar S.K.; Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AY064234; AL51172_1; -; Genomic_DNA.
DR HSSP; P12506; ITBC.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:005634; C:nucleus; IEA.
DR GO; GO:000723; F:RNA binding; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0008350; P:transcription; IEA.
DR InterPro; IPR001831; IV_Tat.
DR Pfam; PF00539; Tat_1.

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OM protein - protein search, using sw model

Run on: August 24, 2006, 23:32:41 ; Search time 39 Seconds (without alignments)

Title: US-10-814-109-2

Perfect score: 107

Sequence: 1 YGRKKBQRQQRKPAASADGHR 20

Scoring table: BloSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*, Maximum Match 100%

Listing first 45 summaries

Database : PIR_80;*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	71.0	71	T09384	trans-activating t
2	71	66.4	86	A25700	trans-activating t
3	71	66.4	86	S33982	trans-activating t
4	71	66.4	95	TNLJ12	trans-activating t
5	71	66.4	101	E44001	trans-activating t
6	71	66.4	101	T09446	tat protein - huma
7	70	65.4	87	T01665	tat protein - huma
8	67	62.6	86	TNLJND	trans-activating t
9	64	59.8	72	TNLJH4	trans-activating t
10	62	57.9	86	TNLJZR	trans-activating t
11	62	57.9	86	JC5591	transactivator prot
12	62	57.9	86	S54381	tat protein - huma
13	53	49.5	953	B70681	probable rne prote
14	50	46.7	371	2	T09466
15	50	46.7	399	2	A39625
16	50	46.7	421	2	C96806
17	50	46.7	541	1	A43610
18	50	46.7	542	1	TVHUSC
19	49	45.8	37	2	S29829
20	49	45.8	367	2	S59329
21	48	44.9	269	2	B38095
22	48	44.9	272	2	A38900
23	48	44.9	303	2	JH0401
24	48	44.9	351	2	T23851
25	48	44.9	453	2	D81870
26	48	44.9	453	2	H81151
27	48	44.9	454	2	E64816
28	48	44.9	455	2	D85588
29	48	44.9	455	2	C90738

ALIGNMENTS

RESULT 1

T09384 trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate F, HIV-1)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Dec-2004

C:Accession: T09384

R:Michael, N.L.; Chang, G.; d'ARCY, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.; Birx, J.; Viroi, 69, 4228-4236, 1995

A:Title: Defective accessory genes in a human immunodeficiency virus type 1-infected long-term culture

A:Reference number: 216654; PMID: 95297475; PMID: 7763682

A:Accession: T09384

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-71 <MIC>

A:Cross-references: UNIPARC:UPI0000FF00C; EMBL:U24451; PIDB: 1-71

A:Gene: tat

C:Superfamily: leukemia virus trans-activating transcription regulator

C:Keywords: transcription

Query Match Score 76; DB 2; Length 71;

Best Local Similarity 65.0%; Pred. No. 0.0014;

Matches 13; Conservative 3; Missmatches 4; Indels 0; Gaps 0;

Qy 1 YGRKKRRRKRKPKASADGHR 20

Db 47 YGRKKRRRKRSPQDSEAHQ 66

RESULT 2

A25700 trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate F, HIV-1)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 31-Dec-2004

C:Accession: A25700

R:Sodroski, J.; Patarca, R.; Rosen, C.; Wong-Staal, P.; Haseltine, W.

A:Reference number: A25700; PMID: 85244627; PMID: 2990041

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-86 <SD>

A:Cross-references: UNIPARC:P04610; UNIPARC:UPI0000111F40

C:Superfamily: leukemia virus trans-activating transcription regulator

Query Match Score 71; DB 2; Length 86;

Best Local Similarity 65.0%; Pred. No. 0.0015;

Matches 13; Conservative 2; Missmatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRRRKRKPKASADGHR 20

Db 47 YGRKKRRRKRSPQGSQTHQ 66

RESULT 3
 S33982 trans-activating transcription regulator - human immunodeficiency virus type 1
 C;Species: human immunodeficiency virus type 1; HIV-1
 C;Date: 06-Oct-1994 #sequence_revision 23-Feb-1996 #text_change 31-Dec-2004
 C;Accession: S33982; S26385; S19864
 R;Carlini, F.
 Submitted to the EMBL Data Library, November 1991
 A;Reference number: S33979
 A;Molecule type: DNA
 A;Residues: 1-86 <CAR>
 A;Cross-references: UNIPROT:P04606; UNIPARC:UPI0000000419; EMBL:Z11530; NID:960192; PIDN
 R;Siderovski, D.P.; Matayama, T.; Frigerio, E.; Chui, S.; Min, X.; Erfle, H.; Sumner-Sm
 Nucleic Acids Res. 20, 5311-5320, 1992
 A;Title: Random mutagenesis of the human immunodeficiency virus type-1 trans-activator c
 A;Reference number: S26385; MUID:93065196; PMID:1437550
 A;Accession: S26385
 A;Molecule type: nucleic acid
 A;Residues: 1-86 <SID>
 A;Cross-references: UNIPARC:UPI0000000419; EMBL:X646550; NID:g60144; PIDN:CAA45921.1; PID
 A;Gene: tat
 A;Introns: 72/2
 C;Superfamily: Leukemia virus trans-activating transcription regulator
 C;Keywords: AIDS; immunodeficiency

Query Match 66.4%; Score 71; DB 2; Length 86;
 Best Local Similarity 65.0%; Pred. No. 0.0075; Indels 0; Gaps 0;
 Matches 13; Conservative 2; Mismatches 5;

Qy 1 YGRKKRQRKRKPASADGHR 20
 Db 47 YGRKKRQRKRQPQGSQTHQ 66

RESULT 6

T09446

tat protein - human immunodeficiency virus type 1 (strain JRF1)

C;Species:

human immunodeficiency virus type 1, HIV-1

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004

C;Accession: T09446

R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,

submitted to the EMBL Data Library, July 1996

A;Reference number: Z16673

A;Accession: T09446

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-101 <PAN>

A;Cross-references: UNIPROT:Q75758; UNIPARC:UPI0000109776; EMBL:U63632; NID:91465777; PIDN

C;Genetics:

A;Gene: tat

A;Introns: 72/2

C;Superfamily: Leukemia virus trans-activating transcription regulator

C;Keywords:

tat protein - human immunodeficiency virus type 1 (strain JRF1)

C;Species:

human immunodeficiency virus type 1, HIV-1

C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 31-Dec-2004

C;Accession: T01665

R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.

Cell 46, 63-74, 1986

A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol

A;Reference number: Z14389; MUID:86245056; PMID:2424612

A;Accession: T01665

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-87 <ALI>

A;Cross-references: UNIPROT:P04613; UNIPARC:UPI00001132A9; EMBL:K03456; NID:g60228; PIDN

C;Genetics:

A;Intronse: 72/2

C;Superfamily: Leukemia virus trans-activating transcription regulator

C;Species:

human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Accession: T01665

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-87 <ALI>

A;Cross-references: UNIPROT:P04613; UNIPARC:UPI00001132A9; EMBL:K03456; NID:g60228; PIDN

C;Genetics:

A;Intronse: 72/2

C;Superfamily: Leukemia virus trans-activating transcription regulator

C;Species:

human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-2004

C;Accession: E44001

R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6537-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties of

A;Reference number: A44001; MUID:93021387; PMID:1404605

A;Accession: E44001

A;Molecule type: DNA

A;Residues: 1-101 <LIV>

A;Cross-references: UNIPROT:P35965; UNIPARC:UPI0000136937; GB:M93258

C;Genetics:

A;Gene: tat

A;Introns: 72/2

C;Superfamily: Leukemia virus trans-activating transcription regulator

C;Keywords: AIDS; immunodeficiency

virus

transcription regulation

C;Species:

human immunodeficiency virus type 1, HIV-1

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 31-Dec-2004

C;Accession: T09446

R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,

submitted to the EMBL Data Library, July 1996

A;Reference number: Z16673

A;Accession: T09446

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-101 <PAN>

A;Cross-references: UNIPROT:Q75758; UNIPARC:UPI0000109776; EMBL:U63632; NID:91465777; PIDN

C;Genetics:

A;Gene: tat

A;Introns: 72/2

C;Superfamily: Leukemia virus trans-activating transcription regulator

C;Keywords:

tat protein - human immunodeficiency virus type 1 (strain JRF1)

C;Species:

human immunodeficiency virus type 1, HIV-1

C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 31-Dec-2004

C;Accession: T01665

R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.

Cell 46, 63-74, 1986

A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol

A;Reference number: Z14389; MUID:86245056; PMID:2424612

A;Accession: T01665

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-87 <ALI>

A;Cross-references: UNIPROT:P04613; UNIPARC:UPI00001132A9; EMBL:K03456; NID:g60228; PIDN

C;Genetics:

A;Intronse: 72/2

C;Superfamily: Leukemia virus trans-activating transcription regulator

C;Species:

human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

Best Local Similarity 65.0%; Pred. No. 0.01; Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;	Qy 1 YGRKRRRKKPASADGHR 20	Db 47 YGRKRRRKKPQQGQAHQ 66	RESULT 8
TN1JND trans-activating transcription regulator - human immunodeficiency virus type 1, HIV-1 C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Dec-2004 C;Accession: JQ0071 R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Batre-Sinoussi, F.; Galibert, F.; Hampe, A.; Gene, 81, 275-284, 1989 A;Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immunodeficiency virus number: JQ0065; MUID:90034200; PMID:2806917 A;Accession: JQ0071 A;Molecule type: DNA A;Residues: 1-86 <SPI> A;Cross-references: UNIPROT:P18804; UNIPARC:UPI000011DSD6; GB:M27323; PID:NID:g328154; PIDN:	Query Match 62.6%; Score 67; DB 1; Length 86; Best Local Similarity 60.0%; Pred. No. 0.036; Matches 12; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	Qy 1 YGRKRRRKKPASADGHR 20 Db 47 YGRKRRRKKPQQGQAHQ 66	RESULT 11 JC5591 transactivator protein - human immunodeficiency virus type 1 C;Alternate names: tat protein C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 31-Dec-2004 C;Accession: JC5591 R;Hoffmann, S.; Willbold, D. Blochem. Biophys. Res. Commun. 235, 806-811, 1997 A;Title: A selection system to study protein-DNA interactions: Functional display of HIV A;Reference number: JC5591; MUID:97350867; PMID:9207243 A;Molecule type: protein A;Residues: 1-86 <HO2> A;Cross-references: UNIPARC:UPI000017865E C;Comment: This protein is a key regulatory protein in the viral replication cycle and be C;Superfamily: leukemia virus trans-activating transcription regulator
F:22-31/Region: cysteine-rich	Query Match 59.9%; Score 62; DB 2; Length 86; Best Local Similarity 60.0%; Pred. No. 0.12; Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;	Qy 1 YGRKRRRKKPASADGHR 20 Db 47 YGRKRRRKKPQQGQTHQ 66	RESULT 12 S54381 trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-2004 C;Accession: B25523 R;Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986 A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human A;Reference number: A94136; MUID:87041461; PMID:3490666 A;Accession: B25523 A;Molecule type: DNA A;Residues: 1-72 <DBS> A;Cross-references: UNIPARC:UPI0000174A55; GB:M13137; NID:g326460
A;Note: the GenBank entry ADRE3AA PID:920908 differs from the published sequence in tra C;Genetics: A;Gene: tat C;Superfamily: leukemia virus trans-activating transcription regulator C;Keywords: transcription regulation	Query Match 59.8%; Score 64; DB 1; Length 72; Best Local Similarity 60.0%; Pred. No. 0.057; Matches 12; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	Qy 1 YGRKRRRKKPASADGHR 20 Db 47 YGRKRRRKKPQQNFIQ 66	RESULT 10 TN1JZR trans-activating transcription regulator - human immunodeficiency virus Zr-6 C;Species: human immunodeficiency virus Zr-6 C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 31-Dec-2004 C;Accession: C26192 R;srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu

A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-399 <WAT>
A; Cross-references: UNIPROT:Q9UUT2; UNIPARC:UPI0000052242
C; Keywords: T-cell receptor
F; 296-371/Domain: HMG box homology <HMG1>

RESULT 13

B70681 probable rne protein - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C; Accession: B70681
R; Cole, S.T.; Broscb, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
i; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Radjandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 53-54, 1998
A; Authors: Spokes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A; Reference number: A70500; MUID:8229587; PMID:9634430
A; Accession: B70681
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-953 <COL>
A; Cross-references: UNIPROT:P71905; UNIPARC:UPI000005011; GB:281451; GB:AL123456; NID:9
C; Experimental source: strain H37RV
C; Genetics:
A; Gene: rne

Query Match 49.5%; Score 53; DB 2; Length 953;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 RKKRQRKRKPASAD 17
Db 230 RRRRRRRRSASGD 244

RESULT 14

B39625 T-cell receptor alpha enhancer-binding protein, short form - human
C; Species: Homo sapiens (man)
C; Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 31-Dec-2004
C; Accession: B39625
R; Waterman, M.L.; Fischer, W.H.; Jones, K.A.
A; Title: A thymus-specific member of the HMG protein family regulates the human T cell
A; Reference number: A39625; MUID:9118420; PMID:201090
A; Accession: B39625
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-371 <WAT>
A; Cross-references: UNIPARC:UPI000017A223
C; Keywords: T-cell receptor
F; 268-343/Domain: HMG box homology <HMG1>

Query Match 46.7%; Score 50; DB 2; Length 371;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKERRQRKPAASDG 18
Db 344 YGKKKRRKREKQESASG 361

RESULT 15

A39625 T-cell receptor alpha enhancer-binding protein, long form - human
C; Species: Homo sapiens (man)
C; Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 31-Dec-2004
C; Accession: A39625
R; Waterman, M.L.; Fischer, W.H.; Jones, K.A.
A; Title: A thymus-specific member of the HMG protein family regulates the human T cell
A; Reference number: A39625; MUID:9118420; PMID:201090
A; Accession: A39625

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OM protein - protein search, using bw model.

Run on: August 24, 2006, 23:39:22 ; Search time 32 Seconds
(without alignments)

Scoring table: BLOSUM62 42.764 Million cell updates/sec

Title: US-10-814-109-2

Perfect score: 107

Sequence: 1 YGRKKRKRRKPKASADGHR 20

Scoring table: Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New:^{*}

1: /EMC_Celerra_SIDS3/ptodata/1/pubpaas/us09_NEW_PUB.PEP:
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaas/us06_NEW_PUB.PEP:
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaas/us07_NEW_PUB.PEP:
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaas/us08_NEW_PUB.PEP:
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaas/oct_NEW_PUB.PEP:
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaas/us10_NEW_PUB.PEP:
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaas/us11_NEW_PUB.PEP:
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaas/us60_NEW_PUB.PEP:
+ Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
US-10-519-677-37

Sequence 37, Application US/10539677
; GENERAL INFORMATION:
; Publication No. US20061049881
; APPLICANT: University of Maryland Biotechnology Institute
; PAUZA, C. David
; ATTORNEY: Tikhonov, Ilia

; TITLE OF INVENTION: VACCINES AGAINST HIV-1 PROTEIN TO GENERATE NEUTRALIZING ANTIBODIES
; FILE REFERENCE: 4115-194
; CURRENT APPLICATION NUMBER: US/10/539,677
; CURRENT FILING DATE: 2005-06-16
; PRIOR APPLICATION NUMBER: US 60/434,368
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 37
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct

RESULT 2
US-10-539-677-37

Query Match 66.4%; Score 71; DB 6; Length 20;
Best Local Similarity 68.4%; Pred. No. 0.002; Indels 4; Mismatches 2; Gaps 0;

Qy 1 YGRKKRKRRKPKASADGH 19
Db 2 YGRKKRKRRKPKASSEDH 20

GENERAL INFORMATION:
; Sequence 6, Application US/11286920
; Publication No. US200616688A1
; APPLICANT: Washington University
; HOCHKISS, Richard
; ATTORNEY: Piwnica-Worms, David
; APPLICANT: McDunn, Jonathan
; TITLE OF INVENTION: Membrane-Permeant Peptide Complexes for Treatment of Sepsis
; FILE REFERENCE: 6000516-0204
; CURRENT APPLICATION NUMBER: US/11/286,920
; CURRENT FILING DATE: 2005-11-23
; PRIOR APPLICATION NUMBER: US 10/374,035

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	71	66.4	20	6	US-10-539-677-37	Sequence 37, App1
2	71	66.4	36	7	US-11-286-920-6	Sequence 6, App1
3	71	66.4	229	6	US-10-533-841-54	Sequence 5, App1
4	71	66.4	293	6	US-10-533-841-52	Sequence 52, App1
5	71	66.4	715	6	US-10-533-841-60	Sequence 60, App1
6	71	66.4	779	6	US-10-533-841-58	Sequence 58, App1
7	71	66.4	1078	6	US-10-533-841-67	Sequence 67, App1
8	71	66.4	1141	6	US-10-533-841-71	Sequence 71, App1
9	71	66.4	1141	6	US-10-533-841-79	Sequence 79, App1
10	71	66.4	1141	6	US-10-533-841-81	Sequence 81, App1
11	71	66.4	1141	6	US-10-533-841-83	Sequence 83, App1
12	71	66.4	1142	6	US-10-533-841-69	Sequence 69, App1
13	71	66.4	1142	6	US-10-533-841-73	Sequence 73, App1
14	71	66.4	1142	6	US-10-533-841-58	Sequence 75, App1
15	71	66.4	1142	6	US-10-533-841-77	Sequence 77, App1
16	70	65.4	20	6	US-10-539-677-36	Sequence 36, App1
17	70	65.4	29	7	US-11-251-734-4	Sequence 4, App1
18	65	60.7	20	6	US-10-539-677-38	Sequence 36, App1
19	64	59.8	14	7	US-11-142-051-4	Sequence 4, App1
20	62	57.9	20	6	US-10-539-677-34	Sequence 34, App1
21	62	57.9	34	7	US-11-223-610-46	Sequence 46, App1
22	61	57.0	20	6	US-10-539-677-35	Sequence 35, App1
23	58	54.2	11	6	US-10-547-530-78	Sequence 78, App1
24	58	54.2	11	6	US-10-518-710-4	Sequence 4, App1
25	58	54.2	11	6	US-10-559-806A-1	Sequence 1, App1

PRIOR FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: US 10/368,280
PRIOR FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 09/557,465
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 09/336,093
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: US 60/090,087
PRIOR FILING DATE: 1998-06-20
PRIOR APPLICATION NUMBER: SEQ ID NOS: 41
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 6
LENGTH: 36
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-11-286-920-6

Query Match 66.4%; Score 71; DB 7; Length 36;
Best Local Similarity 65.0%; Pred. No. 0.0034; 5; Indels 0; Gaps 0;

RESULT 3
US-10-533-841-54
Sequence 54, Application US/10533841
Publication No. US20060142221A1
GENERAL INFORMATION:
APPLICANT: ERTL, Peter F.
TITLE OF INVENTION: Vaccine
FILE REFERENCE: PG5023
CURRENT APPLICATION NUMBER: US/10/533,841
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: PCT/EP 03/12402
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: GB 0225788.9
PRIOR FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 54
LENGTH: 29
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV-1 tNef-Tatm fusion
US-10-533-841-54

Query Match 66.4%; Score 71; DB 6; Length 29;
Best Local Similarity 65.0%; Pred. No. 0.018; 5; Indels 0; Gaps 0;

RESULT 4
US-10-533-841-52
Sequence 52, Application US/10533841
Publication No. US20060142221A1
GENERAL INFORMATION:
APPLICANT: ERTL, Peter F.
TITLE OF INVENTION: Vaccine
FILE REFERENCE: PG5023
CURRENT APPLICATION NUMBER: US/10/533,841
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: PCT/EP 03/12402
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: GB 0225788.9
PRIOR FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 58
LENGTH: 779
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

Query Match 66.4%; Score 71; DB 6; Length 29;
Best Local Similarity 65.0%; Pred. No. 0.018; 5; Indels 0; Gaps 0;

RESULT 5
US-10-533-841-60
Sequence 60, Application US/10533841
Publication No. US20060142221A1
GENERAL INFORMATION:
APPLICANT: ERTL, Peter F.
TITLE OF INVENTION: Vaccine
FILE REFERENCE: PG5023
CURRENT APPLICATION NUMBER: US/10/533,841
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: PCT/EP 03/12402
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: GB 0225788.9
PRIOR FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 60
LENGTH: 715
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV-1 ds-SP120C Nef-Tatm fusion
US-10-533-841-60

Query Match 66.4%; Score 71; DB 6; Length 715;
Best Local Similarity 65.0%; Pred. No. 0.05; 5; Indels 0; Gaps 0;

RESULT 6
US-10-533-841-58
Sequence 58, Application US/10533841
Publication No. US20060142221A1
GENERAL INFORMATION:
APPLICANT: ERTL, Peter F.
TITLE OF INVENTION: Vaccine
FILE REFERENCE: PG5023
CURRENT APPLICATION NUMBER: US/10/533,841
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: PCT/EP 03/12402
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: GB 0225788.9
PRIOR FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 58
LENGTH: 779
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

Query Match 66.4%; Score 71; DB 6; Length 29;
Best Local Similarity 65.0%; Pred. No. 0.018; 5; Indels 0; Gaps 0;

RESULT 7
US-10-533-841-20
Sequence 20, Application US/10533841
Publication No. US20060142221A1
GENERAL INFORMATION:
APPLICANT: ERTL, Peter F.
TITLE OF INVENTION: Vaccine
FILE REFERENCE: PG5023
CURRENT APPLICATION NUMBER: US/10/533,841
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: PCT/EP 03/12402
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: GB 0225788.9
PRIOR FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 89
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 20
LENGTH: 779
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: HIV-1 ds-gp120C' US-10-533-841-58

Query Match Score 71; DB 6; Length 779;
Best Local Similarity 65.0%; Pred. No. 0.054;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
SEQ ID NO: 71 YGRKERRQRRPKPASADGHR 20
Ddb 740 YGRKERRQRRPKPQGSQTHQ 759

RESULT 7
Query Match Score 71; DB 6; Length 1141;
Best Local Similarity 65.0%; Pred. No. 0.054;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
SEQ ID NO: 841-67 YGRKERRQRRPKPASADGHR 20
Ddb 1039 YGRKERRQRRPKPQGSQTHQ 1058

Query Match Score 71; DB 6; Length 1078;
Best Local Similarity 65.0%; Pred. No. 0.073;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
SEQ ID NO: 841-67 YGRKERRQRRPKPASADGHR 20
Ddb 1039 YGRKERRQRRPKPQGSQTHQ 1058

RESULT 8
Query Match Score 71; DB 6; Length 1141;
Best Local Similarity 65.0%; Pred. No. 0.077;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
SEQ ID NO: 71 YGRKERRQRRPKPASADGHR 20
Ddb 1102 YGRKERRQRRPKPQGSQTHQ 1121

OTHER INFORMATION: HIV-1 ds-gp120C' US-10-533-841-58

Query Match Score 71; DB 6; Length 779;
Best Local Similarity 65.0%; Pred. No. 0.054;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
SEQ ID NO: 841-71 YGRKERRQRRPKPASADGHR 20
Ddb 1102 YGRKERRQRRPKPQGSQTHQ 1121

OTHER INFORMATION: HIV-1 ds-gp120C' US-10-533-841-58

Query Match Score 71; DB 6; Length 1141;
Best Local Similarity 65.0%; Pred. No. 0.077;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
SEQ ID NO: 71 YGRKERRQRRPKPASADGHR 20
Ddb 1102 YGRKERRQRRPKPQGSQTHQ 1121

RESULT 11
Query Match Score 71; DB 6; Length 1141;
Best Local Similarity 65.0%; Pred. No. 0.077;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
SEQ ID NO: 841-83 YGRKERRQRRPKPASADGHR 20
Ddb 1102 YGRKERRQRRPKPQGSQTHQ 1121

```

; Sequence 83, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
;   APPLICANT: ERTL, Peter F.
;   TITLE OF INVENTION: Vaccine
;   FILE REFERENCE: PG5023
;   CURRENT APPLICATION NUMBER: US/10/533,841
;   CURRENT FILING DATE: 2005-05-04
;   PRIORITY APPLICATION NUMBER: PCT/EP 03/12402
;   PRIORITY FILING DATE: 2003-03-11
;   PRIORITY APPLICATION NUMBER: GB 0225788.9
;   PRIORITY FILING DATE: 2002-11-05
;   NUMBER OF SEQ ID NOS: 89
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO: 83
;   LENGTH: 1141
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HIV-1 ds-gp120c p17/24 L1-Nef Tatm fusion
US-10-533-841-83

Query Match          66.4%;  Score 71;  DB 6;  Length 1141;
Best Local Similarity 65.0%;  Pred. No. 0.077;  Mismatches 5;  Indels 0;  Gaps 0;
Matches 13;  Conservative 2;  Mismatches 5;  Indels 0;  Gaps 0;

RESULT 12           US-10-533-841-69
; Sequence 69, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
;   APPLICANT: ERTL, Peter F.
;   TITLE OF INVENTION: Vaccine
;   FILE REFERENCE: PG5023
;   CURRENT APPLICATION NUMBER: US/10/533,841
;   CURRENT FILING DATE: 2005-05-04
;   PRIORITY APPLICATION NUMBER: PCT/EP 03/12402
;   PRIORITY FILING DATE: 2003-03-11
;   PRIORITY APPLICATION NUMBER: GB 0225788.9
;   PRIORITY FILING DATE: 2002-11-05
;   NUMBER OF SEQ ID NOS: 89
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO: 69
;   LENGTH: 1142
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HIV-1 ds-gp120c p17/24 Nef Tatm fusion
US-10-533-841-69

Query Match          66.4%;  Score 71;  DB 6;  Length 1142;
Best Local Similarity 65.0%;  Pred. No. 0.077;  Mismatches 5;  Indels 0;  Gaps 0;
Matches 13;  Conservative 2;  Mismatches 5;  Indels 0;  Gaps 0;

RESULT 13           US-10-533-841-73
; Sequence 73, Application US/10533841
; Publication No. US20060142221A1
; GENERAL INFORMATION:
;   APPLICANT: ERTL, Peter F.
;   TITLE OF INVENTION: Vaccine
;   FILE REFERENCE: PG5023
;   CURRENT APPLICATION NUMBER: US/10/533,841
;   CURRENT FILING DATE: 2005-05-04
;   PRIORITY APPLICATION NUMBER: PCT/EP 03/12402
;   PRIORITY FILING DATE: 2003-03-11
;   PRIORITY APPLICATION NUMBER: GB 0225788.9
;   PRIORITY FILING DATE: 2002-11-05
;   NUMBER OF SEQ ID NOS: 89
;   SOFTWARE: FastSEQ for Windows Version 4.0

```

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; SEQ ID NO: 77
; LENGTH: 1142
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-1 ds-gp120c p17/24 LL-NeF Tact fusion
US-10-533-841-77

Query Match          66.4%; Score 71; DB 6; Length 1142;
Best Local Similarity 65.0%; Pred. No. 0.077;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 YGRKRRRKRDKASADGHR 20
Db     1103 YGRKRRRKRDKASADGHRQSGSQTHQ 1122

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OM protein - protein search, using sw model.

Run on: August 24, 2006, 23:38:27 ; Search time 185 Seconds (without alignments)

50.079 Million cell updates/sec

Title: US-10-814-109-2

Precise score: 107

Sequence: 1 YGRKIKRQRKKPASADGHR 20

Scoring table: BL0SUM62

Gappen 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% ; Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main.*
 1: /EMC_Celerra_SIDS3_ptoata/2/pubpaas/US07_PUBCOMB.pep;*
 2: /EMC_Celerra_SIDS3_ptoata/2/pubpaas/US08_PUBCOMB.pep;*
 3: /EMC_Celerra_SIDS3_ptoata/2/pubpaas/US09_PUBCOMB.pep;*
 4: /EMC_Celerra_SIDS3_ptoata/2/pubpaas/US10A_PUBCOMB.pep;*
 5: /EMC_Celerra_SIDS3_ptoata/2/pubpaas/US10B_PUBCOMB.pep;*
 6: /EMC_Celerra_SIDS3_ptoata/2/pubpaas/US11_PUBCOMB.pep;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	100.0	20	5 US-10-814-109-2	Sequence 2, Appli
2	79	73.8	101	4 US-10-190-435-211	Sequence 2,1, Appli
3	78	72.9	101	4 US-10-190-435-220	Sequence 2,1, Appli
4	78	72.9	101	5 US-10-780-507-110	Sequence 11,0, Appli
5	75	70.1	101	4 US-10-190-435-227	Sequence 22,7, Appli
6	75	70.1	101	6 US-11-205-883A-6	Sequence 6, Appli
7	75	70.1	1896	4 US-10-296-734-393	Sequence 393, Appli
8	75	70.1	5747	4 US-10-296-734-405	Sequence 405, Appli
9	74	69.2	101	4 US-10-190-435-213	Sequence 213, Appli
10	74	69.2	101	5 US-10-501-223-1	Sequence 1, Appli
11	74	69.2	101	5 US-10-501-223-20	Sequence 20, Appli
12	74	69.2	101	5 US-10-501-223-21	Sequence 21, Appli
13	74	69.2	101	5 US-10-501-223-42	Sequence 22, Appli
14	74	69.2	101	5 US-10-501-223-41	Sequence 41, Appli
15	74	69.2	101	5 US-10-501-223-42	Sequence 42, Appli
16	74	69.2	101	5 US-10-501-223-43	Sequence 43, Appli
17	74	69.2	101	5 US-10-501-223-74	Sequence 74, Appli
18	73	68.2	101	6 US-11-135-597-219	Sequence 219, Appli
19	73	68.2	102	4 US-10-770-668-50	Sequence 50, Appli
20	73	68.2	1893	4 US-10-296-734-399	Sequence 399, Appli
21	72	67.3	99	4 US-10-190-435-215	Sequence 215, Appli
22	72	67.3	99	4 US-10-190-435-218	Sequence 218, Appli
23	72	67.3	100	5 US-10-969-191-16	Sequence 16, Appli
24	72	67.3	101	4 US-10-190-435-208	Sequence 208, Appli
25	72	67.3	101	4 US-10-190-435-210	Sequence 210, Appli
26	72	67.3	101	4 US-10-190-435-212	Sequence 212, Appli
27	72	67.3	101	4 US-10-190-435-216	Sequence 216, Appli

ALIGNMENTS

RESULT 1
 US-10-814-109-2

; Sequence 2, Application US/10814109
 ; Publication No. US20050224042A1

; GENERAL INFORMATION:
 ; APPLICANT: Salter, Michael
 ; INVENTOR: Gingrich, Jeffrey
 ; TITLE OF INVENTION: Method For Modification of NMDA Receptors Through Inhibition of S, T, and Cysteine Residues
 ; FILE REFERENCE: 2560_004
 ; CURRENT APPLICATION NUMBER: US/10/814_109
 ; CURRENT FILING DATE: 2004-03-30
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 2
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Query Match 100.0%; Score 107; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5e-08; Mismatches 0; Indels 0; Gaps 0;
 US-10-814-109-2

Qy 1 YGRKIKRQRKKPASADGHR 20
 Db 1 YGRKIKRQRKKPASADGHR 20

RESULT 2
 US-10-190-435-211

; Sequence 211, Application US/10190435
 ; Publication No. US20030143248A1

; GENERAL INFORMATION:
 ; APPLICANT: ZUR MEGEDE, Jan W.
 ; INVENTOR: BARNETT, Susan W.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C POLYPEPTIDES, POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
 ; FILE REFERENCE: PP/8133-003 / 2302-18133
 ; CURRENT APPLICATION NUMBER: US/10/190_435
 ; CURRENT FILING DATE: 2002-12-30
 ; NUMBER OF SEQ ID NOS: 319
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 211

Query Match 100.0%; Score 107; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5e-08; Mismatches 0; Indels 0; Gaps 0;
 US-10-190-435-211

Qy 1 YGRKIKRQRKKPASADGHR 20
 Db 1 YGRKIKRQRKKPASADGHR 20

; OTHER INFORMATION: Description of Artificial Sequence: Tat TV006
 US-10-190-435-211

Query Match Score 79; DB 4; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0019; Indels 0; Gaps 0;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRKPASADGHR 20
 Db 47 YGRKKRQRRSTPPSSEGHQ 66

RESULT 3
 US-10-190-435-221
 ; Sequence 221, Application US/10190435
 ; Publication No. US20030143248A1

; GENERAL INFORMATION:
 ; APPLICANT: ZUR MEGEDE, Jan
 ; APPLICANT: BARNETT, Susan W.
 ; APPLICANT: LIAN, Ying
 ; APPLICANT: ENGELBRECHT, Susan
 ; APPLICANT: VAN RENSBURG, Estrelita J.

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
 ; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
 ; FILE REFERENCE: PP1813.003 / 2302-18133

; CURRENT APPLICATION NUMBER: US10/190,435
 ; CURRENT FILING DATE: 2002-12-30
 ; NUMBER OF SEQ ID NOS: 319
 ; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 221
 ; LENGTH: 101
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Tat 301904-Ind
 ; US-10-190-435-221

Query Match Score 78; DB 4; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0026; Indels 0; Gaps 0;
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRKPASADGHR 20
 Db 47 YGRKKRQRRAPQSSDHQ 66

RESULT 4
 US-10-780-507-110
 ; Sequence 110, Application US/10780507
 ; Publication No. US20050137387A1

; GENERAL INFORMATION:
 ; APPLICANT: MULLINS, James I.
 ; APPLICANT: RODRIGO, Allen G.
 ; APPLICANT: LEARN, Gerald H.
 ; APPLICANT: LI, Fusheng
 ; APPLICANT: NICKLE, David C.
 ; APPLICANT: JENSEN, Mark A.

; TITLE OF INVENTION: ANCESTRAL AND COT VIRAL SEQUENCES, PROTEINS AND IMMUNOGENIC COMPOUNDS
 ; FILE REFERENCE: 16336-00120US
 ; CURRENT APPLICATION NUMBER: US/10/780,507
 ; CURRENT FILING DATE: 2004-02-17
 ; PRIOR APPLICATION NUMBER: US 10/204,204
 ; PRIOR FILING DATE: 2001-02-16
 ; PRIOR APPLICATION NUMBER: PCT/US01/05283
 ; PRIOR FILING DATE: 2001-02-16
 ; PRIOR APPLICATION NUMBER: US 60/183,659
 ; PRIOR FILING DATE: 2000-02-18
 ; PRIOR APPLICATION NUMBER: US 60/447,586
 ; PRIOR FILING DATE: 2003-02-14
 ; NUMBER OF SEQ ID NOS: 125
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 110
 ; LENGTH: 101

; TYPE: PRT ; Artificial sequence
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Most recent common ancestor reconstructions of clade C tat protein
 ; OTHER INFORMATION: n sequence
 ; US-10-780-507-110

Query Match Score 78; DB 5; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0026; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRKPASADGHR 20
 Db 47 YGRKKRQRRAPQSSDHQ 66

RESULT 5
 US-10-190-435-227
 ; Sequence 227, Application US/10190435
 ; Publication No. US20030143248A1

; GENERAL INFORMATION:
 ; APPLICANT: ZUR MEGEDE, Jan
 ; APPLICANT: BARNETT, Susan W.
 ; APPLICANT: LIAN, Ying
 ; APPLICANT: ENGELBRECHT, Susan
 ; APPLICANT: VAN RENSBURG, Estrelita J.

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
 ; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
 ; FILE REFERENCE: PP1813.003 / 2302-18133
 ; CURRENT APPLICATION NUMBER: US/10/190,435
 ; CURRENT FILING DATE: 2002-12-30
 ; NUMBER OF SEQ ID NOS: 319
 ; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 227
 ; LENGTH: 101
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Tat C2220-Beth

; PEPTIDE; NAME/KEY: SITE
 ; LOCATION: (40)
 ; OTHER INFORMATION: where Xaa = unknown amino acid

Qy 1 YGRKKRQRRKPASADGHR 20
 Db 47 YGRKKRQRRAPQSSDHQ 66

Query Match Score 75; DB 4; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.007; Indels 0; Gaps 0;

Qy 1 YGRKKRQRRKPASADGHR 20
 Db 47 YGRKKRQRRAPQSSDHQ 66

RESULT 6
 US-11-205-883A-6
 ; Sequence 6, Application US/11205883A

; GENERAL INFORMATION:
 ; APPLICANT: PAYNE, SHELLIE M.
 ; APPLICANT: DUDLEY, JAQUELINE P.
 ; APPLICANT: SELIGER, STEPHAN S.
 ; APPLICANT: FENG, ZHENGYU

; TITLE OF INVENTION: BACTERIAL VECTOR SYSTEMS
 ; FILE REFERENCE: CLPR-030US
 ; CURRENT APPLICATION NUMBER: US/11/205,883A
 ; CURRENT FILING DATE: 2005-08-17
 ; PRIOR APPLICATION NUMBER: 60/602,276
 ; PRIOR FILING DATE: 2004-08-17
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 101

TYPE: PRT ; ORGANISM: Artificial Sequence ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: Peptide US-11-205-88JA-6

Query Match 70.1%; Score 75; DB 6; Length 101; Best Local Similarity 70.0%; Pred. No. 0.007; Indels 4; Gaps 0; Matches 14; Conservative 2; Mismatches 4; Indexes 0; Gaps 0;

Qy 1 YGRKKRRQRRKPASADGHR 20
Db 47 YGRKKRRQRRTPQSSKDHQ 66

RESULT 7
US-10-296-734-393
Sequence 393, Application US/10296734
Publication No. US20040054137A1.
GENERAL INFORMATION:
APPLICANT: Thompson, Scott A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU PQ7761/00
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: PatentIn version 3.2
SEQ ID NO 393
LENGTH: 1896

TYPE: PRT ; ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: HIV cassette A1 US-10-296-734-393

Query Match 70.1%; Score 75; DB 4; Length 1896; Best Local Similarity 70.0%; Pred. No. 0.11; Indels 4; Gaps 0; Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRKPASADGHR 20
Db 186 YGRKKRRQRRPQSSKDHQ 205

RESULT 8
US-10-296-734-405
Sequence 405, Application US/10296734
Publication No. US20040054137A1.
GENERAL INFORMATION:
APPLICANT: Thompson, Scott A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU PQ7761/00
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: PatentIn version 3.2
SEQ ID NO 405
LENGTH: 5747

TYPE: PRT ; ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: HIV complete bovine US-10-296-734-405

Query Match 70.1%; Score 75; DB 4; Length 5747; Best Local Similarity 70.0%; Pred. No. 0.31; Indels 0; Gaps 0;

Qy 1 YGRKKRRQRRKPASADGHR 20
Db 47 YGRKKRRQRRPQSSKDHQ 66

RESULT 9
US-10-190-435-213
Sequence 213, Application US/10190435
Publication No. US2003014348A1
GENERAL INFORMATION:
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: BARNETT, Susan W.
APPLICANT: LIAN, Ying
APPLICANT: ENGELBRECHT, Susan J.
APPLICANT: VAN RENSBURG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: PPI18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 213
TYPE: PRT ; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Tat TV008 US-10-190-435-213

Query Match 69.2%; Score 74; DB 4; Length 101; Best Local Similarity 65.0%; Pred. No. 0.0096; Mismatches 3; Indexes 0; Gaps 0;

Qy 1 YGRKKRRQRRKPASADGHR 20
Db 47 YGRKKRRQRRPQSSBDHQ 66

RESULT 10
US-10-301-223-1
Sequence 1, Application US/10501223
Publication No. US2005016416A1
GENERAL INFORMATION:
APPLICANT: GUILLON, CHRISTOPHE
APPLICANT: CHEDAL-BORNU, AURELIE
APPLICANT: VERRIER, BERNARD
TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS
FILE REFERENCE: 0508-1107
CURRENT APPLICATION NUMBER: US/10/501,223
CURRENT FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: PCT/FR03/00051
PRIOR FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: FR 02/00319
SEQ ID NO 1
LENGTH: 101
TYPE: PRT ; ORGANISM: Human immunodeficiency virus type 1 US-10-301-223-1

Query Match 69.2%; Score 74; DB 5; Length 101; Best Local Similarity 65.0%; Pred. No. 0.0096; Mismatches 3; Indexes 0; Gaps 0;

Qy 1 YGRKKRRQRRKPASADGHR 20
Db 47 YGRKKRRQRRPQSSDETHQ 66

RESULT 11
US-10-501-223-20
Sequence 20, Application US/10501223
; Publication No. US20050164164A1
GENERAL INFORMATION:
; APPLICANT: GUILLOIN, CHRISTOPHE
; APPLICANT: CHEDAL-BORNU, AURELIE
; APPLICANT: VERRIER, BERNARD
; APPLICANT: MANDRAND, BERNARD
TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS
FILE REFERENCE: 0508-1107
CURRENT APPLICATION NUMBER: US/10/501,223
CURRENT FILING DATE: 2004-07-12
PRIORITY NUMBER: PCT/FR03/00051
PRIOR FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: FR 02/00319
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 141
SOFTWARE: PatentIn version 3.3
SEQ ID NO 20
LENGTH: 101
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G79A-K89L
; OTHER INFORMATION: mutant of Tat protein
US-10-501-223-20

Query Match 69.2%; Score 74; DB 5; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.0096;
Matches 13; Conservative 3; N mismatches 4; Indels 0; Gaps 0;
Qy 1 YGRKERRQRRKPASADGHR 20
Db 47 YGRKERRQRRKPASADGHR 66

RESULT 12
US-10-501-223-21
Sequence 21, Application US/10501223
; Publication No. US20050164164A1
GENERAL INFORMATION:
; APPLICANT: GUILLOIN, CHRISTOPHE
; APPLICANT: CHEDAL-BORNU, AURELIE
; APPLICANT: VERRIER, BERNARD
; APPLICANT: MANDRAND, BERNARD
TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS
FILE REFERENCE: 0508-1107
CURRENT APPLICATION NUMBER: US/10/501,223
CURRENT FILING DATE: 2004-07-12
PRIORITY NUMBER: PCT/FR03/00051
PRIOR FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: FR 02/00319
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 141
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21
LENGTH: 101
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G79A-E92Q
; OTHER INFORMATION: mutant of Tat protein
US-10-501-223-21

Query Match 69.2%; Score 74; DB 5; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.0096;
Matches 13; Conservative 3; N mismatches 4; Indels 0; Gaps 0;

RESULT 13
US-10-501-223-22
Sequence 22, Application US/10501223
; Publication No. US20050164164A1
GENERAL INFORMATION:
; APPLICANT: GUILLOIN, CHRISTOPHE
; APPLICANT: CHEDAL-BORNU, AURELIE
; APPLICANT: VERRIER, BERNARD
; APPLICANT: MANDRAND, BERNARD
TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS
FILE REFERENCE: 0508-1107
CURRENT APPLICATION NUMBER: US/10/501,223
CURRENT FILING DATE: 2004-07-12
PRIORITY NUMBER: PCT/FR03/00051
PRIOR FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: FR 02/00319
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 141
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22
LENGTH: 101
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: K89L-E92Q
; OTHER INFORMATION: mutant of Tat protein
US-10-501-223-22

Query Match 69.2%; Score 74; DB 5; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.0096;
Matches 13; Conservative 3; N mismatches 4; Indels 0; Gaps 0;

RESULT 14
US-10-501-223-41
Sequence 41, Application US/10501223
; Publication No. US20050164164A1
GENERAL INFORMATION:
; APPLICANT: GUILLOIN, CHRISTOPHE
; APPLICANT: CHEDAL-BORNU, AURELIE
; APPLICANT: VERRIER, BERNARD
; APPLICANT: MANDRAND, BERNARD
TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS
FILE REFERENCE: 0508-1107
CURRENT APPLICATION NUMBER: US/10/501,223
CURRENT FILING DATE: 2004-07-12
PRIORITY NUMBER: PCT/FR03/00051
PRIOR FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: FR 02/00319
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 141
SOFTWARE: PatentIn version 3.3
SEQ ID NO 41
LENGTH: 101
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C27S-G79A-K89L
; OTHER INFORMATION: mutant of Tat protein
US-10-501-223-41

Query Match 69.2%; Score 74; DB 5; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.0096;
Matches 13; Conservative 3; N mismatches 4; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRKPASADGHR 20

Db 47 YGRKRRQRRSPQDSETHQ 66

RESULT 15

| Sequence 42, Application US/10501223
| Publication No. US20050164164A1.
| GENERAL INFORMATION:
| | APPLICANT: GUILLOU, CHRISTOPHE
| | APPLICANT: CHEDAL-BORNU, AURELIE
| | APPLICANT: VERRIER, BERNARD
| | APPLICANT: MANDRAND, BERNARD
| | TITLE OF INVENTION: HIV-1 VIRUS TAT PROTEIN MUTANTS
| | FILE REFERENCE: 050-1107
| | CURRENT APPLICATION NUMBER: US/10/501,223
| | CURRENT FILING DATE: 2004-07-12
| | PRIOR APPLICATION NUMBER: PCT/FR03/00051.
| | PRIOR FILING DATE: 2003-01-09
| | PRIOR APPLICATION NUMBER: FR 02/00319
| | PRIOR FILING DATE: 2002-01-11
| | SOFTWARE: PatentIn version 3.3
| | SEQ ID NO 42
| | LENGTH: 101
| | TYPE: PRT
| | ORGANISM: Artificial Sequence
| | FEATURE:
| | OTHER INFORMATION: Description of Artificial Sequence: C27S-G79A-E92Q
| | OTHER INFORMATION: mutant of rat protein
US-10-501-223-42

Query Match Score 74; DB 5; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.0096;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YGRKRRQRRKPASADGHR 20
Db 47 YGRKRRQRRSPQDSETHQ 66

Search completed: August 24, 2006, 23:42:19
Job time : 186 secs

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OM protein - protein search, using sw model

Run on: August 24, 2006, 23:37:42 ; Search time 50 Seconds
(without alignments)

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : Issued Patents AA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	73	68.2	101	2	US-10-290-579A-219	Sequence 219, App
2	72	67.3	101	2	US-09-475-515-86	Sequence 86, App
3	72	67.3	101	2	US-10-290-579A-223	Sequence 223, App
4	72	67.3	101	2	US-10-290-579A-224	Sequence 224, App
5	72	67.3	101	2	US-10-290-579A-226	Sequence 226, App
6	72	67.3	102	2	US-09-475-515-90	Sequence 90, App
7	71	66.4	26	1	US-09-450-257-48	Sequence 48, App
8	71	66.4	26	1	US-08-450-246-48	Sequence 48, App
9	71	66.4	26	1	US-08-450-098-48	Sequence 48, App
10	71	66.4	26	1	US-08-451-233-48	Sequence 48, App
11	71	66.4	26	1	US-08-450-236-48	Sequence 48, App
12	71	66.4	26	1	US-08-335-401-48	Sequence 49, App
13	71	66.4	35	1	US-08-450-257-49	Sequence 2, App
14	71	66.4	35	1	US-08-450-246-49	Sequence 49, App
15	71	66.4	35	1	US-08-450-098-49	Sequence 49, App
16	71	66.4	35	1	US-08-451-233-49	Sequence 49, App
17	71	66.4	35	1	US-08-450-236-49	Sequence 49, App
18	71	66.4	35	1	US-08-335-401-49	Sequence 49, App
19	71	66.4	36	1	US-08-450-257-52	Sequence 2, App
20	71	66.4	36	1	US-08-450-246-52	Sequence 2, App
21	71	66.4	36	1	US-08-450-098-52	Sequence 2, App
22	71	66.4	36	1	US-08-451-233-52	Sequence 2, App
23	71	66.4	36	1	US-08-450-236-52	Sequence 2, App
24	71	66.4	36	2	US-09-113-921-55	Sequence 55, App
25	71	66.4	36	2	US-08-235-403-52	Sequence 2, App
26	71	66.4	36	2	US-09-336-093-56	Sequence 6, App

ALIGNMENTS

RESULT 1
US-10-290-579A-219
; Sequence 219, Application US/10290579A

; Patent No. 6887301 ; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice
; APPLICANT: Gao, Feng
; APPLICANT: Shaw, George
; TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
; FILE REFERENCE: D6287D
; CURRENT APPLICATION NUMBER: US/10/290,579A
; PRIORITY FILING DATE: 2002-11-08
; PRIORITY APPLICATION NUMBER: US 09/184,418
; PRIORITY FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 270
; SEQ ID NO 219
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: isolate=92RM009_6; gene=tat
; US-10-290-579A-219

Query Match 68.1%; Score 73; DB 2; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.00052;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YGRKIKRQRREKKPASADGHR 20
Db 47 YGRKIKRQRREKKPASSEDHQ 66

RESULT 2
US-09-475-515-86
; Sequence 86, Application US/09475515A
; Patent No. 6602705 ; GENERAL INFORMATION:
; APPLICANT: ZUR MBEGDE, Jan
; APPLICANT: SRIVASTAVA, Indresh
; APPLICANT: LIAN, Ying
; APPLICANT: HARTOG, Karin
; APPLICANT: LIU, Hong
; APPLICANT: GREER, Catherine
; APPLICANT: SELBY, Mark
; APPLICANT: WALKER, Christopher
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
; TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES

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; FILE REFERENCE: 1621.002
; CURRENT APPLICATION NUMBER: US/09/475,515A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 86
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-475-515-86

Query Match 67.3% Score 72; DB 2; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.00074; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
RESULT 5
US-10-290-579A-226
; Sequence 226, Application US/10290579A
; Patent No. 6897301
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice
; APPLICANT: Gao, Feng
; TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
; FILE REFERENCE: D6287D
; CURRENT APPLICATION NUMBER: US/10/290,579A
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 09/184,418
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 270
; SEQ ID NO: 226
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: isolate=96ZM751.3; gene=tat
US-10-290-579A-226

Query Match 67.3% Score 72; DB 2; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.00074; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
RESULT 6
US-09-475-515-90
; Sequence 90, Application US/09475515A
; Patent No. 6602705
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: SRIVASTAVA, Indresh
; APPLICANT: LIAN, Ying
; APPLICANT: HARTOG, Karin
; APPLICANT: LIU, Hong
; APPLICANT: GREER, Catherine
; APPLICANT: SELBY, Mark
; APPLICANT: WALKER, Christopher
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
; FILE REFERENCE: 1621.002
; CURRENT APPLICATION NUMBER: US/09/475,515A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 90
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tat cyb22

Query Match 67.3% Score 72; DB 2; Length 101;
Best Local Similarity 65.0%; Pred. No. 0.00074; Indels 0; Gaps 0;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
RESULT 4
US-10-290-579A-224
; Sequence 224, Application US/10290579A
; Patent No. 6897301
; GENERAL INFORMATION:
; APPLICANT: Hahn, Beatrice
; APPLICANT: Gao, Feng
; APPLICANT: Shaw, George
; TITLE OF INVENTION: CLONES AND SEQUENCES FOR NON-SUBTYPE B ISOLATES OF HUMAN
; FILE REFERENCE: D6287D
; CURRENT APPLICATION NUMBER: US/10/290,579A
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 09/184,418
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 270
; SEQ ID NO: 224
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: tat cyb22

```

OTHER INFORMATION: SF162 protein
US-09-475-515-90

Query Match Score 72%; DB 2; Length 102;
Best Local Similarity 65.0%; Pred. No. 0.00074;
Matches 13; Conservative 3; Mismatches 4; Indels 0;
Gaps 0;

Qy 1 YGRKKRKRRRKPAASDGH 20
Db 47 YGRKKRKRRRKPAAPDSEVHQ 66

RESULT 7
US-08-450-257-48
Sequence 48, Application US/08450257

PATENT NO. 5652122
GENERAL INFORMATION:

APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.

TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10020
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,257

FILING DATE: 25-MAY-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/235,403

FILING DATE: 28-APR-1994

APPLICATION NUMBER: US 07/934,375

FILING DATE: 21-AUG-1993

APPLICATION NUMBER: PCT/US93/07833

FILING DATE: 19-AUG-1993

APPLICATION NUMBER: US 07/454,450

FILING DATE: 21-DEC-1992

APPLICATION NUMBER: US 07/454,450

FILING DATE: 28-JUL-1993

APPLICATION NUMBER: PCT/US93/07833

FILING DATE: 02-JAN-1991

APPLICATION NUMBER: US 08/158,015

FILING DATE: 24-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr., James F.

REGISTRATION NUMBER: 27,794
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9090
TELEFAX: (212) 596-9090

TELEX: 14-8367
SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
TOPOLOGY: linear

SEQUENCE FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
TOPOLOGY: linear

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
TOPOLOGY: linear

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
TOPOLOGY: linear

Best Local Similarity 65.0%; Pred. No. 0.00027;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRKRRRKPAASDGH 20
Db 1 YGRKKRKRRRKPAASDGH 20

RESULT 8
US-08-450-246-48

Sequence 48, Application US/08450246

PATENT NO. 5670617
GENERAL INFORMATION:

APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl

APPLICANT: BARSOUM, James G.

APPLICANT: FAWELL, Stephen E.

APPLICANT: PEPINSKY, R. B.

TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10020
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,246

FILING DATE: 25-MAY-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/235,403

FILING DATE: 28-APR-1994

APPLICATION NUMBER: US 07/934,375

FILING DATE: 21-AUG-1992

APPLICATION NUMBER: PCT/US93/07833

FILING DATE: 19-AUG-1993

APPLICATION NUMBER: US 07/454,450

FILING DATE: 21-DEC-1992

APPLICATION NUMBER: US 07/636,662

FILING DATE: 24-NOV-1993

APPLICATION NUMBER: US 08/158,015

FILING DATE: 21-DEC-1992

APPLICATION NUMBER: US 07/636,662

FILING DATE: 24-NOV-1993

APPLICATION NUMBER: US 08/158,015

FILING DATE: 21-DEC-1992

APPLICATION NUMBER: US 07/636,662

FILING DATE: 24-NOV-1993

APPLICATION NUMBER: US 08/158,015

FILING DATE: 24-NOV-1993

APPLICATION NUMBER: US 07/636,662

FILING DATE: 24-NOV-1993

APPLICATION NUMBER: US 08/158,015

FILING DATE: 24-NOV-1993

Best Local Similarity 65.0%; Pred. No. 0.00027;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRKRRRKPAASDGH 20
Db 1 YGRKKRKRRRKPAASDGH 20

RESULT 8
US-08-450-246-48

Sequence 48, Application US/08450246

PATENT NO. 5670617
GENERAL INFORMATION:

APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl

APPLICANT: BARSOUM, James G.

APPLICANT: FAWELL, Stephen E.

APPLICANT: PEPINSKY, R. B.

TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10020
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,246

FILING DATE: 25-MAY-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/235,403

FILING DATE: 28-APR-1994

APPLICATION NUMBER: US 07/934,375

FILING DATE: 21-AUG-1992

APPLICATION NUMBER: PCT/US93/07833

FILING DATE: 19-AUG-1993

APPLICATION NUMBER: US 07/454,450

FILING DATE: 21-DEC-1992

APPLICATION NUMBER: US 07/636,662

FILING DATE: 24-NOV-1993

APPLICATION NUMBER: US 08/158,015

FILING DATE: 24-NOV-1993

Best Local Similarity 65.0%; Pred. No. 0.00027;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRKRRRKPAASDGH 20
Db 1 YGRKKRKRRRKPAASDGH 20

RESULT 9
US-08-450-257-48

Sequence 48, Application US/08450257

PATENT NO. 5670617
GENERAL INFORMATION:

APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl

APPLICANT: BARSOUM, James G.

APPLICANT: FAWELL, Stephen E.

APPLICANT: PEPINSKY, R. B.

TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10020
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,257

FILING DATE: 25-MAY-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/235,403

FILING DATE: 28-APR-1994

APPLICATION NUMBER: US 07/934,375

FILING DATE: 21-AUG-1992

APPLICATION NUMBER: PCT/US93/07833

FILING DATE: 19-AUG-1993

APPLICATION NUMBER: US 07/454,450

FILING DATE: 21-DEC-1992

APPLICATION NUMBER: US 07/636,662

FILING DATE: 24-NOV-1993

APPLICATION NUMBER: US 08/158,015

Db ||||| : 1 YGRKERRQRRRPPQGQHQ 20

RESULT 9
US-08-450-098-48
; Sequence 48, Application US/08450098
; Patent No. 5574980
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10020
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1993
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-450-098-48

Cy Query Match 66.4%; Score 71; DB 1; Length 26;
Best Local Similarity 65.0%; Pred. No. 0.00027; Mismatches 5; Indels 0; Gaps 0;

Db Query 1 YGRKERRQRRRPPQGQHQ 20
; Sequence 48, Application US/08450236
; Patent No. 5804604

RESULT 10
US-08-451-233-48
; Sequence 48, Application US/08451233
; Patent No. 5747641
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,233
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-451-233-48

Query Match 66.4%; Score 71; DB 1; Length 26;
Best Local Similarity 65.0%; Pred. No. 0.00027; Mismatches 5; Indels 0; Gaps 0;

Db Query 1 YGRKERRQRRRPPQGQHQ 20
; Sequence 48, Application US/08450236
; Patent No. 5804604

RESULT 11
US-08-450-236-48
; Sequence 48, Application US/08450236
; Patent No. 5804604

GENERAL INFORMATION:
 APPLICANT: FRANKEL, Alan
 APPLICANT: PABO, Carl
 APPLICANT: BARSOUM, James G.
 APPLICANT: FAWELL, Stephen E.
 APPLICANT: PEPINSKY, R. B.
 TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & NEAVE
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10020

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/450,236
 FILING DATE: 25-MAY-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/235,403
 FILING DATE: 28-APR-1994
 APPLICATION NUMBER: US 07/934,375
 FILING DATE: 21-AUG-1992
 APPLICATION NUMBER: US 07/098,766
 FILING DATE: 28-JUL-1993
 APPLICATION NUMBER: PCT/US93/07833
 FILING DATE: 19-AUG-1993
 APPLICATION NUMBER: US 07/454,450
 FILING DATE: 21-DEC-1992
 APPLICATION NUMBER: US 07/636,662
 FILING DATE: 02-JAN-1991
 APPLICATION NUMBER: US 08/158,015
 FILING DATE: 24-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: B170 CIP 2
 TELECOMMUNICATION INFORMATION:
 APPLICATION NUMBER: US 08/158,015
 FILING DATE: 24-NOV-1993
 APPLICATION NUMBER: US 07/454,450
 FILING DATE: 21-DEC-1992
 APPLICATION NUMBER: US 07/636,662
 FILING DATE: 02-JAN-1991
 APPLICATION NUMBER: US 08/158,015
 FILING DATE: 24-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: B170 CIP 2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEX: 14-8367
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-450-236-48

Query Match Score 66.4%; Pred. No. 0.00027; Length 26;
 Best Local Similarity 65.0%; Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

RESULT 12
 US-08-450-235-48
 Sequence 48, Application US/08235403
 Patent No. 6316003

GENERAL INFORMATION:
 APPLICANT: FRANKEL, Alan
 APPLICANT: PABO, Carl
 APPLICANT: BARSOUM, James G.
 APPLICANT: FAWELL, Stephen E.
 APPLICANT: PEPINSKY, R. B.
 TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & NEAVE

STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10020
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/450,257
 FILING DATE: 25-MAY-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/235,403
 FILING DATE: 28-APR-1994
 APPLICATION NUMBER: US 07/934,375
 FILING DATE: 21-AUG-1992
 APPLICATION NUMBER: US 07/098,766
 FILING DATE: 28-JUL-1991
 APPLICATION NUMBER: PCT/US93/07833
 FILING DATE: 19-AUG-1993
 APPLICATION NUMBER: US 07/934,375
 FILING DATE: 21-AUG-1993
 APPLICATION NUMBER: US 07/098,766
 FILING DATE: 28-JUL-1991
 APPLICATION NUMBER: PCT/US93/07833
 FILING DATE: 19-AUG-1993
 APPLICATION NUMBER: US 07/454,450
 FILING DATE: 21-DEC-1990
 APPLICATION NUMBER: US 07/636,662
 FILING DATE: 02-JAN-1991
 APPLICATION NUMBER: US 08/158,015
 FILING DATE: 24-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Haley Jr., James F.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: B170 CIP 2
 TELECOMMUNICATION INFORMATION:
 NAME: Haley Jr., James F.
 REFERENCE/DOCKET NUMBER: 27,794
 TELEPHONE: (212) 596-9000
 TELEX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-450-257-49

Query Match 66.4%; Score 71; DB 1; Length 35;
 Best Local Similarity 65.0%; Pred. No. 0.00036; Mismatches 5; Indels 0; Gaps 0;
 Matches 13; Conservative 2; Gaps 0; Gaps 0;

Qy 1 YGRKERRQRRKKPASADGHR 20
 Db 10 YGRKERRQRRKKPASADGHR 20

RESULT 15
 US-08-450-098-49

Sequence 49, Application US/08450098
 Patent No. 5670617
 GENERAL INFORMATION:
 APPLICANT: FRANKEL, Alan
 APPLICANT: PABO, Carl
 APPLICANT: BARSUM, James G.
 APPLICANT: FAWELL, Stephen E.
 APPLICANT: PEPINSKY, R. B.
 TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & NEAVE
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA

RESULT 14
 US-08-450-246-49

Sequence 49, Application US/08450246
 Patent No. 5670617
 GENERAL INFORMATION:
 APPLICANT: FRANKEL, Alan
 APPLICANT: PABO, Carl
 APPLICANT: BARSUM, James G.
 APPLICANT: FAWELL, Stephen E.
 APPLICANT: PEPINSKY, R. B.
 TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & NEAVE
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James P.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-450-098-49

Query Match 66.4%; Score 71; DB 1; Length 35;
Best Local Similarity 65.0%; Pred. No. 0.00036;
Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 YGRKKRRKRPASADGHR 20
Db 10 YGRKKRRKRPQQGSQTHQ 29

Search completed: August 24, 2006, 23:39:08
Job time : 51 secs

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Copyright (c) 1993 - 2006 Biocceleration Ltd.
DOM protein - protein search, using sw model
Run on: August 24, 2006, 23:28:36 ; Search time 196 Seconds
 (without alignments)
 46.655 Million cell updates/sec
Title: US-10-814-109-2
Penfект score: 107
Sequence: 1 YGRKRRQRRRPASADGHR 20
Scoring table: BLOSUM62
Gapext: 0.5
Number of hits searched: 2589679 seqs, 45716429 residues
Total number of hits satisfying chosen parameters: 2589679

ALIGNMENTS

RESULT 1											
Database :		AED21152 standard; peptide; 20 AA.									
ID :		AED21152									
XX		XX									
AC :		AED21152;									
XX		XX									
DT :		01-DEC-2005									
XX		XX									
DE :		SUDAPI-1/ HIV Tat domain fusion peptide, TSUDAPI-1 SEQ ID NO: 2.									
XX		XX									
KW		Protein interaction; therapeutic; cerebrovascular ischemia; multiple sclerosis; cerebroprotective; vasotropics; hypoxia; ischemia; neurotropic; neuroprotective; Huntington's chorea; anticonvulsant; nootropic; parkinsons disease; antiparkinsonian; Alzheimer's disease; hyperglycemia; antidiabetic; diabetes; trauma; tranquilizer; pulmonary; epilepsy; grand mal seizure; muscle hypertonia; muscle relaxant; paralysis; muscular-gen.; asthma; antiasthmatic; cardiac arrest; cardiac disorder; macular degeneration; ophthalmological; psychiatric disorder; neuroleptic; schizophrenia; AIDS dementia complex; dementia; inflammation; antiinflammatory; pain; analgesic; opiate dependence; ant-addictive; cocaine addiction; alcoholism; antialcoholic; anorexia nervosa; anabolic; eating-disorders-gen.;									
KW		Src-unique domain anchoring protein inhibitor.									
XX		XX									
OS		Homo sapiens.									
OS		Human immunodeficiency virus.									
XX		XX									
FH		Location/Qualifiers									
FT		1..11									
FT		/note= "HIV transduction domain (TAT)"									
FT		12..20									
FT		/note= "Src unique domain anchoring protein inhibitor 1"									
XX		XX									
PN		US20052222042-A1.									
XX		XX									
PD		06-OCT-2005.									
XX		XX									
PF		30-MAR-2004; 2004US-00814109.									
XX		XX									
PR		30-MAR-2004; 2004US-00814109.									
XX		XX									
PA		(HOSP-) HOSPITAL FOR SICK CHILDREN RES INST.									
XX		XX									
PI		Salter MW, Gingrich JR;									
XX		XX									
DR		WPT: 2005-689427/71									
Maximum Match:		100%									
Listing first 45 summaries											
SUMMARIES											
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.											
Result No.	Score	Query Match	Length	DB	ID						
1	107	100.0	20	9	AED21152	Aed21152 SUDAPI-1/					
2	80	74.8	101	9	ADX40278	Adx40278 HIV Tat P					
3	78	72.9	100	9	ADX40269	Adx40269 HIV Tat P					
4	78	72.9	101	9	ADX40367	Adx40367 HIV Tat P					
5	78	72.9	101	9	ADX40406	Adx40406 HIV Tat P					
6	78	72.9	101	9	AEB10643	Aeb10643 Claude C t					
7	77	72.0	101	9	ADX40408	Adx40408 HIV Tat P					
8	77	72.0	101	9	ADX40398	Adx40398 HIV Tat P					
9	75	70.1	72	2	AAR10515	Aar10515 ARV tat S					
10	75	70.1	100	9	ADX40365	Adx40365 HIV Tat P					
11	75	70.1	101	9	ADX40316	Adx40316 HIV Tat P					
12	75	70.1	101	9	ADX40407	Adx40407 HIV Tat P					
13	75	70.1	101	9	ADX40319	Adx40319 HIV Tat P					
14	75	70.1	102	9	ADX40285	Adx40285 HIV Tat P					
15	75	70.1	1896	5	AAU84590	Aau84590 HIV Cassie					
16	75	70.1	5746	5	AAU84596	Aau84596 HIV comp1					
17	74	69.2	101	9	ADX40347	Adx40347 HIV Tat P					
18	74	69.2	101	9	ADX40289	Adx40289 HIV Tat P					
19	74	69.2	101	9	ADX40343	Adx40343 HIV Tat P					
20	74	69.2	101	9	ADX40401	Adx40401 HIV Tat P					
21	73	68.2	101	3	AAB89315	Aab89315 HIV-1 non					
22	73	68.2	101	9	ADX40288	Adx40288 HIV Tat P					
23	73	68.2	101	9	ADX40324	Adx40324 HIV Tat P					

XX Modifying N-methyl-D-aspartate receptor interaction with non-receptor
PT tyrosine kinase Src in cells, comprises administering composition
PT comprising Src-unique domains anchoring protein inhibitor to cells.
XX

Claim 13; SEQ ID NO 2; 32pp; English.

XX The present invention provides a method for modifying N-methyl-D-
CC aspartate receptor (NMDAR) interaction with non-receptor tyrosine kinase
CC Src in cells. The method involves administering a composition including
CC at least one Src-unique domain anchoring protein inhibitor (SUDAPI) to
CC the cells, where modification ameliorates a disease or condition related
CC to NMDAR signaling. Diseases or conditions ameliorated by the invention
CC include stroke, hypoxia, ischemia, multiple sclerosis, Huntington's
CC chorea, Parkinson's disease, Alzheimer's disease, hyperglycemia,
CC diabetes, traumatic injury, epilepsy, grand mal seizures, spasticity,
CC cerebral palsy, asthma, cardiac arrest, macular degeneration, mental,
CC diseases, schizophrenia, AIDS dementia complex, other dementias, AIDS
CC wasting syndrome, inflammation, pain, opioid addiction, cocaine addiction,
CC alcohol, addiction and other conditions associated with substance abuse
CC and anorexia. The present sequence is the SUDAPI-I/HIV Tat domain fusion
CC peptide, TSUDAPI-I.

XX Sequence 20 AA;

Query Match 100.0%; Score 107; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e-08; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Del 0; Insert 0;

Qy 1 YGRRKRRRKRPAASADGHR 20
Db 1 YGRRKRRRKRPAASADGHR 20

RESULT 2
ADX40278 standard; protein; 101 AA.
XX

Qy ADX40278;
Db 21-APR-2005 (first entry)

DE HIV Tat protein #20.

XX Immune stimulation; Tat.
KW Human immunodeficiency virus.
OS

PN WO2005012502-A2.

XX 10-FEB-2005.

XX 29-MAR-2004; 2004WO-US009510.
PR 28-MAR-2003; 2003US-0458026P.

PA (EPIM-) EPIMMUNE INC.

PI Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;

DR XX

WPI; 2005-132661/14.

XX Identifying a candidate peptide epitope, which induces a HLA class I CTL
PT response against variants of a peptide epitope 8-11 amino
PT acids in length comprising primary anchor residues of the same HLA class
PT I binding motif.
XX Disclosure; Page 333-338; 458pp; English.

XX The invention relates to a method of identifying a candidate peptide
CC epitope which induces an HLA class I CTL response against variants of the
CC peptide epitope, comprising identifying variants of a peptide epitope comprising primary anchor
CC infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class
CC I binding motif.

CC residues of the same HLA class I binding motif. The method is useful for
CC identifying a candidate peptide epitope, which induces an HLA class I CTL
CC response against variants of the peptide epitope. This sequence
CC represents an HIV Tat protein used in the scope of the invention.
XX

SQ Sequence 101 AA;

Query Match 74.8%; Score 80; DB 9; Length 101;
Best Local Similarity 70.0%; Pred. No. 0.00062; Indels 0; Gaps 0;
Matches 14; Conservative 3; Mismatches 3; Del 0; Insert 0;

Qy 1 YGRRKRRRKRPAASADGHR 20
Db 47 YGRRKRRRKRPAASSEAHQ 66

RESULT 3
ADX40269 standard; protein; 100 AA.
ID ADX40269;
XX AC ADX40269;
XX DT 21-APR-2005 (first entry)
XX DE HIV Tat protein #11.

XX Immune stimulation; Tat.

XX Human immunodeficiency virus.

PN WO2005012502-A2.

XX PD 10-FEB-2005.

XX PR 29-MAR-2004; 2004WO-US009510.

XX PR 28-MAR-2003; 2003US-0458026P.

PA (EPIM-) EPIMMUNE INC.

PI Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;

DR XX

WPI; 2005-132661/14.

XX Identifying a candidate peptide epitope, which induces a HLA class I CTL
CC response against variants of a peptide epitope 8-11 amino
CC acids in length comprising primary anchor residues of the same HLA class
CC I binding motif. The method is useful for
CC identifying a candidate peptide epitope, which induces an HLA class I CTL
CC response against variants of the peptide epitope. This sequence
CC represents an HIV Tat protein used in the scope of the invention.
XX

SQ Sequence 100 AA;

Query Match 72.9%; Score 78; DB 9; Length 100;
Best Local Similarity 70.0%; Pred. No. 0.0012; Indels 0; Gaps 0;
Matches 14; Conservative 3; Mismatches 3; Del 0; Insert 0;

Qy 1 YGRRKRRRKRPAASADGHR 20
Db 47 YGRRKRRRKRPAASSEHQ 66

RESULT 4
ADX40367

XX The invention relates to an ancestral or center of tree (COT) viral
 CC nucleic acid and amino acid sequences that are determined founder
 CC sequences of a highly diverse viral strain. The invention also relates to
 CC a composition comprising a highly diverse viral ancestor protein or an
 CC immunogenic fragment of an ancestor or COT protein for inducing an immune
 CC response in mammal and a method for preparing an ancestral or COT viral
 CC amino acid sequence. The composition and methods are useful for
 CC diagnosing, preventing or treating viral (e.g. HIV) infection. The
 CC invention is also useful in gene therapy. The present sequence is a clade
 CC C tat protein. This sequence is used in the comparison of the most recent
 CC common ancestor (MRCA), COT least squares (LScot) and COT minimum of
 CC means (MMcot) reconstructions for the Clade C tat gene.

XX SQ Sequence 101 AA;

Query Match 72.9%; Score 78; DB 9; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0012; Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRKPKASADGHR 20

Db 47 YGRKERRQRRRTPQSQAHQ 66

RESULT 7
 ADX40408 ID ADX40408 standard; protein: 101 AA.
 XX ADX40408;
 XX DR 21-APR-2005 (first entry)
 XX DE HIV Tat protein #150.
 XX Immune stimulation; Tat.
 XX Human immunodeficiency virus.
 XX OS WO2005012502-A2.
 XX PN WO2005012502-A2.
 XX PD 10-FEB-2005.
 XX PR 29-MAR-2004; 2004WO-US009510.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;
 XX XY Disclosure; Page 333-338; 458pp; English.
 XX DR WPI; 2005-132661/14.
 XX PR 28-MAR-2003; 2003US-0458026P.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;
 XX DR Disclosure; Page 333-338; 458pp; English.
 XX PR 28-MAR-2004; 2004WO-US009510.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;
 XX DR WPI; 2005-132661/14.
 XX PR 28-MAR-2003; 2003US-0458026P.
 XX PA (EPIM-) EPIMMUNE INC.
 XX PI Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;
 XX DR Disclosure; Page 335-340; 458pp; English.

CC The invention relates to a method of identifying a candidate peptide
 CC epitope which induces an HLA class I CTL response against variants of the
 CC peptide epitope, comprising identifying, from a particular antigen of an
 CC infectious agent, variants of a peptide epitope comprising primary anchor
 CC residues of the same HLA class I binding motif. The method is useful for
 CC identifying a candidate peptide epitope, which induces an HLA class I CTL
 CC response against variants of the peptide epitope. This sequence
 CC represents an HIV Tat protein used in the scope of the invention.

XX SQ Sequence 101 AA;

Query Match 72.0%; Score 77; DB 9; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0017; Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRKPKASADGHR 20

Db 47 YGRKERRQRRSAPASSEDHQ 66

RESULT 9

AAR10515 ID AAR10515 standard; protein: 72 AA.
 XX AC AAR10515;
 XX DT 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)
 XX DT 04-APR-1991 (first entry)

DE ARV tat gene product.

XX The invention relates to an ancestral or center of tree (COT) viral
 CC nucleic acid and amino acid sequences that are determined founder
 CC sequences of a highly diverse viral strain. The invention also relates to
 CC a composition comprising a highly diverse viral ancestor protein or an
 CC immunogenic fragment of an ancestor or COT protein for inducing an immune
 CC response in mammal and a method for preparing an ancestral or COT viral
 CC amino acid sequence. The composition and methods are useful for
 CC diagnosing, preventing or treating viral (e.g. HIV) infection. The
 CC invention is also useful in gene therapy. The present sequence is a clade
 CC C tat protein. This sequence is used in the comparison of the most recent
 CC common ancestor (MRCA), COT least squares (LScot) and COT minimum of
 CC means (MMcot) reconstructions for the Clade C tat gene.

XX SQ Sequence 101 AA;

Qy 1 YGRKERRQRRKPKASADGHR 20

Db 47 YGRKERRQRRRTPQSQAHQ 66

RESULT 8

ADX40298 ID ADX40298 standard; protein: 101 AA.

XX AC ADX40298;

XX DT 21-APR-2005 (first entry)

XX DE HIV Tat protein #40.

XX KW Immune stimulation; Tat.

XX Human immunodeficiency virus.

Qy 1 YGRKERRQRRKPKASADGHR 20

Db 47 YGRKERRQRRRTPQSSEDHQ 66

RESULT 9

ADX40408 ID ADX40408 standard; protein: 101 AA.

XX ADX40408;

XX DR 21-APR-2005 (first entry)

XX DE HIV Tat protein #150.

XX Immune stimulation; Tat.

XX Human immunodeficiency virus.

Qy 1 YGRKERRQRRKPKASADGHR 20

Db 47 YGRKERRQRRRTPQSQAHQ 66

The invention relates to a method of identifying a candidate peptide
 CC epitope which induces an HLA class I CTL response against variants of the
 CC peptide epitope, comprising identifying, from a particular antigen of an
 CC infectious agent, variants of a peptide epitope comprising primary anchor
 CC residues of the same HLA class I binding motif. The method is useful for
 CC identifying a candidate peptide epitope, which induces an HLA class I CTL
 CC response against variants of the peptide epitope. This sequence
 CC represents an HIV Tat protein used in the scope of the invention.

XX SQ Sequence 101 AA;

Query Match 72.0%; Score 77; DB 9; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0017; Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRKERRQRRKPKASADGHR 20

Db 47 YGRKERRQRRSAPASSEDHQ 66

RESULT 9

AAR10515 ID AAR10515 standard; protein: 72 AA.

XX AC AAR10515;

DT 25-MAR-2003 (revised)
 XX DT 10-MAR-2003 (revised)
 XX DT 04-APR-1991 (first entry)

DE ARV tat gene product.

XX Human T-cell leukaemia virus; HTLV-III; acquired immune deficiency; AIDS;
 KW transactivation; LAV.
 XX OS Human immunodeficiency virus.
 XX PN US4981790-A.
 XX PD 01-JAN-1991.
 XX PF 06-DEC-1985; 85US-00806263.
 XX PR 25-MAY-1984; 84US-00614297.
 XX PA (DAND) DANA FARBER CANCER INST INC.
 XX PS Disclosure: Fig 7; 16pp; English.
 XX The sequence is that of the tatIII gene product, which regulates gene
 CC expression directed by the HTLV-III/LAV long terminal repeat. See also
 CC AAR10511-14. (Updated on 10-MAR-2003 to add missing OS field.) (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX SQ Sequence 72 AA;
 Query Match 70.1%; Score 75; DB 2; Length 72;
 Best Local Similarity 70.0%; Pred. No. 0.0024; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 YGRKKRKRRRKPAASADGHR 20
 Db 47 YGRKKRKRRRKPAASADGHR 66

RESULT 10
 ADX40365
 ID ADX40365 standard; protein; 100 AA.
 XX ADX40365;
 XX DT 21-APR-2005 (first entry)
 XX DE HIV Tat protein #107.
 XX KW Immune stimulation; Tat.
 XX OS Human immunodeficiency virus.
 XX PN WO2005012502-A2.

Query Match 70.1%; Score 75; DB 2; Length 72;
 Best Local Similarity 70.0%; Pred. No. 0.0024; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 YGRKKRKRRRKPAASADGHR 20
 Db 47 YGRKKRKRRRKPAASADGHR 66

RESULT 11
 ADX40316
 ID ADX40316 standard; protein; 101 AA.
 XX AC ADX40316;
 XX DT 21-APR-2005 (first entry)
 XX DE HIV Tat protein #58.
 XX KW Immune stimulation; Tat.
 XX OS Human immunodeficiency virus.
 XX PN WO2005012502-A2.

Query Match 70.1%; Score 75; DB 9; Length 100;

Best Local Similarity 70.0%; Pred. No. 0.0033; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 YGRKKRKRRRKPAASADGHR 20
 Db 46 YGRKKRKRRRKPAASADGHR 65

Query Match 70.1%; Score 75; DB 9; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0033; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 YGRKKRKRRRKPAASADGHR 20
 Db 47 YGRKKRKRRRKPAASADGHR 66

XX Human T-cell leukaemia virus; HTLV-III; acquired immune deficiency; AIDS;
 KW transactivation; LAV.
 XX OS Human immunodeficiency virus.

The invention relates to a method of identifying a candidate peptide
 CC epitope which induces an HLA class I CTL response against variants of the
 CC peptide epitope, comprising identifying, from a particular antigen of an
 CC infectious agent, variants of a peptide epitope comprising primary anchor
 CC residues of the same HLA class I binding motif. The method is useful for
 CC identifying a candidate peptide epitope, which induces an HLA Class I CTL
 CC response against variants of the peptide epitope. This sequence
 CC represents an HIV Tat protein used in the scope of the invention.
 XX SQ Sequence 100 AA;

Query Match 70.1%; Score 75; DB 9; Length 100;
 Best Local Similarity 70.0%; Pred. No. 0.0033; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 YGRKKRKRRRKPAASADGHR 20
 Db 46 YGRKKRKRRRKPAASADGHR 65

RESULT 11
 ADX40316
 ID ADX40316 standard; protein; 101 AA.

XX AC ADX40316;

XX DT 21-APR-2005 (first entry)
 XX DE HIV Tat protein #58.

XX KW Immune stimulation; Tat.

XX OS Human immunodeficiency virus.

XX PN WO2005012502-A2.

XX PD 10-FEB-2005.

XX PR 29-MAR-2004; 2004WO-US009510.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ;

XX DR WPI; 2005-132661/14.

XX PS Disclosure: Page 333-339; 458pp; English.
 XX The invention relates to a method of identifying a candidate peptide
 CC epitope which induces an HLA class I CTL response against variants of the
 CC peptide epitope, comprising identifying, from a particular antigen of an
 CC infectious agent, variants of a peptide epitope comprising primary anchor
 CC residues of the same HLA class I binding motif. The method is useful for
 CC identifying a candidate peptide epitope, which induces an HLA Class I CTL
 CC response against variants of the peptide epitope. This sequence
 CC represents an HIV Tat protein used in the scope of the invention.
 XX SQ Sequence 101 AA;

Query Match 70.1%; Score 75; DB 9; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0033; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Query Match 70.1%; Score 75; DB 9; Length 101;
 Best Local Similarity 70.0%; Pred. No. 0.0033; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy	1 YGRKKRRKRPASADGHR 20 47 YGRKKRRKRPASADGHR 66	OS Human immunodeficiency virus. XX WO2005012502-A2.	
Db		XX PN XX PD 10-FEB-2005. XX PR 29-MAR-2004; 2004WO-US009510. XX PF 28-MAR-2003; 2003US-0458026P. XX PR 28-MAR-2003; 2003US-0458026P.	
RESULT 12 ADX40407 ID ADX40407 standard; protein; 101 AA. XX AC ADX40407; DT 21-APR-2005 (first entry) XX DB HIV Tat protein #149. XX KW Immune stimulation; Tat. XX OS Human immunodeficiency virus. XX PN WO2005012502-A2. XX PR 10-FEB-2005. XX PF 29-MAR-2004; 2004WO-US009510. XX PR 28-MAR-2003; 2003US-0458026P. XX PR (EPIM-) EPIMMUNE INC. XX PI Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ; XX WPI; 2005-132661/14. XX PS Disclosure; Page 333-339; 458pp; English.	XX The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HIV Tat protein used in the scope of the invention. XX SQ Sequence 101 AA: XX Query Match 70.1%; Score 75; DB 9; Length 101; Best Local Similarity 70.0%; Pred. No. 0.0033; Mismatches 2; Indels 4; Gaps 0; Gapg 0; Matches 14; Conservative 2; MisMatches 4; Indels 0; Gaps 0; XX Qy 1 YGRKKRRKRPASADGHR 20 Db 47 YGRKKRRKRPASADGHR 66		
Qy	1 YGRKKRRKRPASADGHR 20 47 YGRKKRRKRPASADGHR 66	RESULT 14 ADX40285 standard; protein; 102 AA. XX AC ADX40285; DT 21-APR-2005 (first entry) XX DB HIV Tat protein #27. XX KW Immune stimulation; Tat. XX OS Human immunodeficiency virus. XX PN WO2005012502-A2. XX PR 10-FEB-2005. XX PF 29-MAR-2004; 2004WO-US009510. XX PR 28-MAR-2003; 2003US-0458026P. XX PR (EPIM-) EPIMMUNE INC. XX PI Baker DM, Livingston BD, Chesnut RW, Sette A, Newman MJ; XX WPI; 2005-132661/14. XX PS Identifying a candidate peptide epitope, which induces a HLA class I CTL response comprises identifying variants of a peptide epitope 8-11 amino acids in length comprising primary anchor residues of the same HLA Class I binding motif.	XX The invention relates to a method of identifying a candidate peptide epitope which induces an HLA class I CTL response against variants of the peptide epitope, comprising identifying, from a particular antigen of an infectious agent, variants of a peptide epitope comprising primary anchor residues of the same HLA class I binding motif. The method is useful for identifying a candidate peptide epitope, which induces an HLA class I CTL response against variants of the peptide epitope. This sequence represents an HIV Tat protein used in the scope of the invention. XX SQ Sequence 101 AA: XX Query Match 70.1%; Score 75; DB 9; Length 101; Best Local Similarity 70.0%; Pred. No. 0.0033; Mismatches 2; Indels 4; Gaps 0; Gapg 0; Matches 14; Conservative 2; MisMatches 4; Indels 0; Gaps 0; XX Qy 1 YGRKKRRKRPASADGHR 20 Db 47 YGRKKRRKRPASADGHR 66
Qy	1 YGRKKRRKRPASADGHR 20 47 YGRKKRRKRPASADGHR 66	RESULT 13 ADX0319 standard; protein; 101 AA. XX AC ADX0319; DT 21-APR-2005 (first entry) XX DB HIV Tat protein #61. XX KW Immune stimulation; Tat.	XX The invention relates to a method of identifying a candidate peptide epitope, which induces an HLA class I CTL response comprises identifying variants of a peptide epitope 8-11 amino acids in length comprising primary anchor residues of the same HLA Class I binding motif.

PT acids in length comprising primary anchor residues of the same HLA class
 PR I binding motif.
 XX Disclosure: Page 333-338; 458pp; English.

XX The invention relates to a method of identifying a candidate peptide
 CC epitope which induces an HLA class I CTL response against variants of the
 CC peptide epitope, comprising identifying, from a particular antigen of an
 CC infectious agent, variants of a peptide epitope comprising primary anchor
 CC residues of the same HLA class I binding motif. The method is useful for
 CC identifying a candidate peptide epitope, which induces an HLA class I CTL
 CC response against variants of the peptide epitope. This sequence
 CC represents an HIV Tat protein used in the scope of the invention.

XX Sequence 102 AA;

Query Match 70.1%; Score 75; DB 9; Length 102;
 Best Local Similarity 65.0%; Pred. No. 0.0034; Indels 0; Gaps 0;
 Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGRKKRKRRRKPAASDGH 20
 Db 47 YGRKKRKRRRSAPSSSENHQ 66

RESULT 15

AAU84590 standard; protein; 1896 AA.

AAU84590;

AC 08-MAY-2002 (first entry)

XX HIV Cassette A1 Protein.

XX WO20010197-A1.

XX PN 29-NOV-2001.

XX PP 25-MAY-2001; 2001WO-AU000622.

XX PR 26-MAY-2000; 2000AU-00007761.

XX PA (AUSU) UNIV AUSTRALIAN NAT.

XX PI Thomson SA, Ramshaw IA;

XX DR WPI: 2002-147575/19.

DR N-PSDB, ABK36429.

XX PS XX ID NO 393; 364pp; English.

The invention relates to a new synthetic polypeptide (I) comprising

several different segments of at least one parent polypeptide linked
 together in a different relationship relative to their linkage in the
 parent polypeptide to impede, abrogate or otherwise alter at least one
 function associated with the parent polypeptide and for inducing an
 immune response against a pathogen or cancer. Also included are asynthetic polynucleotide encoding and computer system for designing the
 synthetic polypeptides. The synthetic polypeptides and polynucleotides

CC are referred to as a Savine. The synthetic polypeptide is useful for
 CC modulating immune responses preferably directed against a pathogen or a
 CC cancer. (e.g., cancers of the lung, breast, ovary, cervix, colon, head
 CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
 CC oesophagus, brain, testicle, uterus), as potentiating agents.
 CC Compositions comprising the polypeptide may be used in the treatment or
 CC prophylaxis against viral (such as infections caused by HIV (human
 CC immunodeficiency virus), hepatitis, Japanese encephalitis, bacterial
 CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
 CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
 CC Salmonella, Streptococcal, Legionella and Mycobacteria, Leishmania,
 CC (e.g., infections caused by Plasmodium, Schistosoma, Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
 CC a cassette protein consisting of several peptides derived from a parent
 CC protein. One or more cassettes are used to construct a savine of the
 CC invention

XX Sequence 1896 AA;
 SQ Query Match 70.1%; Score 75; DB 5; Length 1896;
 Best Local Similarity 70.0%; Pred. No. 0.05;
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YGRKKRKRRRKPAASDGH 20
 Db 186 YGRKKRKRRRSAPSSSENHQ 205

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